MyEIM User Manual

Environmental Information Management

Washington State Department of Ecology
 • email: myeim@ecy.wa.gov • October 2015 Edition

Table of Contents

MyEIM Disclaimer:

Extensive efforts have been made to develop and test MyEIM tools and to verify that the EIM data met the EIM data submittal business rules. However, MyEIM tools and contents are subject to change per regulatory and non-regulatory criteria updates, EIM data updates and MyEIM tool updates. Neither Ecology nor any of their employees makes any warranty or assumes any legal liability or responsibility for the accuracy or completeness of the data searched or analyzed by MyEIM tools. It is the responsibility of the user to ensure that the searched and analyzed data using MyEIM tools meet the user's needs.

Preface: Introduction to MyEIM

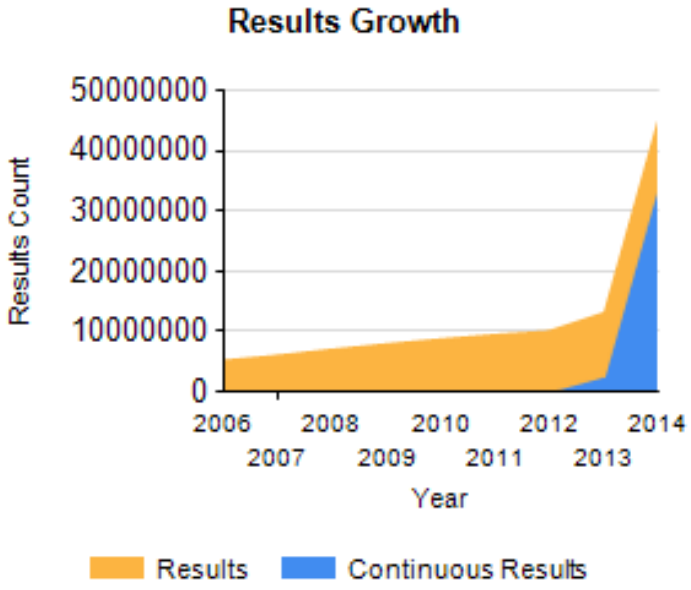
MyEIM is a search, mapping and analysis tool for the data in EIM. More overview sections for EIM and MyEIM are provided below.

ABOUT EIM

The **Environmental Information Management System (EIM)** is the Washington Department of Ecology's (Ecology's) main database for environmental monitoring data. EIM contains records on physical, chemical, biological, and habitat analyses and measurements. EIM centers on three main elements – Study, Locations, and Results (including Bioassay, Well Water Levels, and Time-Series data). Supplementary information about the data (metadata) is also stored, including information about environmental studies, monitoring locations, and data quality.

Ecology staff collecting EIM data from the air, land, and water

EIM grew from 1 million discrete records in 2002 to 11 million discrete records and 34.5 million time-series (continuous) records as of fall 2014. For more information on EIM, go to http://www.ecy.wa.gov/eim/ (Public site). Ecology staff should go to http://aww.ecology/eim/eim_home.htm.



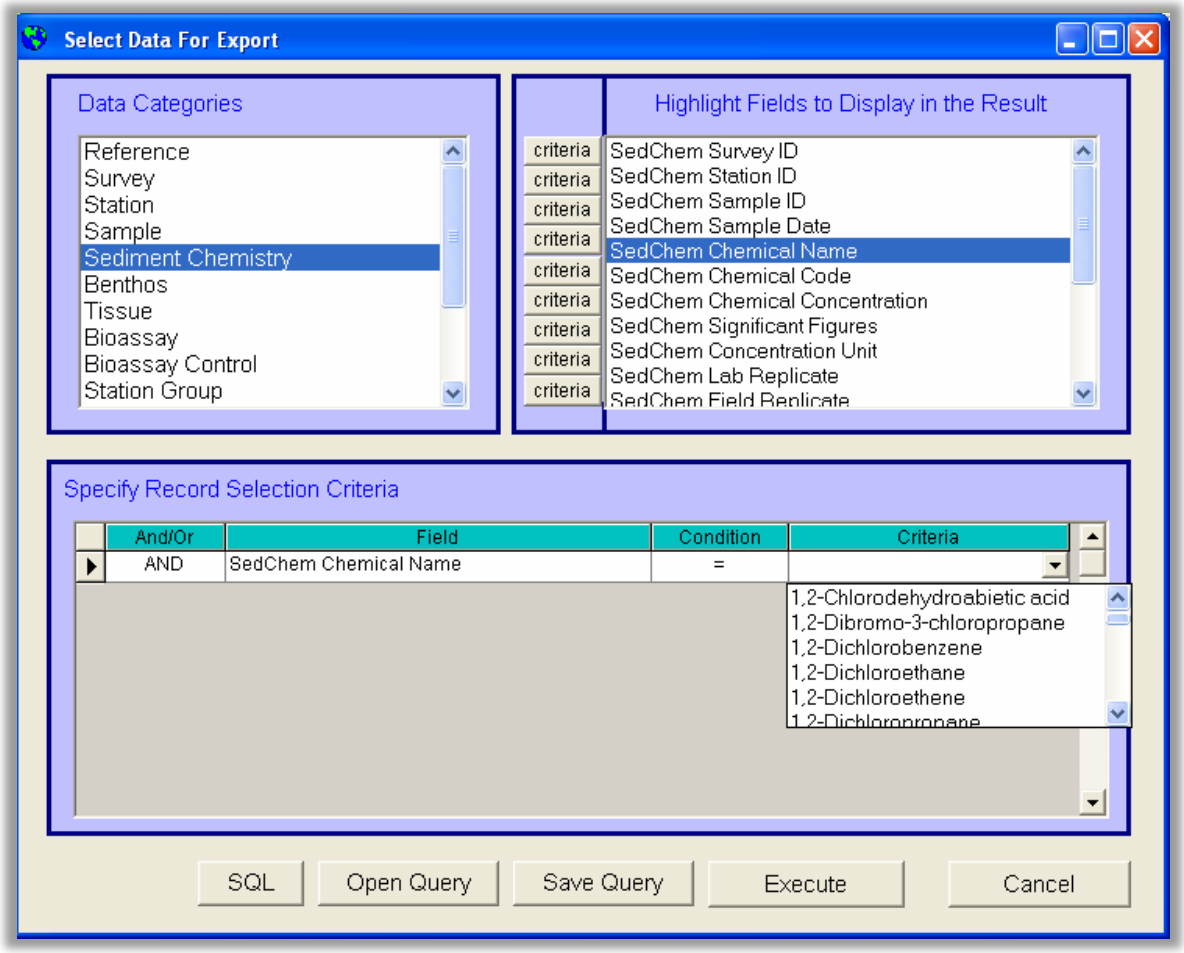
EIM Applications

EIM is a system made up of several applications that allow you to upload, edit, search, map, and download data. EIM also provides help on many topics.

Application Name	Website Address
EIM Help System Look up EIM field names and descriptions, search EIM reference tables, or contact us for help.	https://fortress.wa.gov/ecy/eimreporting/Help/HelpFieldSearch.aspx (Public) http://ecyeim/search/Help/HelpFieldSearch.aspx (Ecology staff)
EIM Loader Submit/Load EIM data.	http://www.ecy.wa.gov/eim/submitData.htm (Public) http://ecyeim/loader/ (Ecology staff)
EIM Editor Modify EIM data.	http://ecyeim/editor/ (Ecology staff only)
EIM Search Search EIM data by form or by map; download or map data.	https://fortress.wa.gov/ecy/eimreporting/ (Public) http://ecyeim/search/(Ecology staff)

OVERVIEW OF MYEIM

In 2007, MyEIM / EIM replaced SEDQUAL, Ecology's old sediment-specific standalone database, search and analysis tool, with a modern web-based search, mapping and analysis application that harnessed the power of the EIM system.



SEDQUAL Home Page

MyEIM is more powerful than the standard EIM Search. MyEIM allows you to:

1. search any EIM fields, EIM predefined groups and custom groups using your selected search criteria ,
2. create, save and share your searches, custom groups, user defined derived variables and user defined cleanup criteria,

3. process your searched chemistry data by
    a. normalizing your searched results to the same units of your selected comparison cleanup criteria,
    b. aggregating your searched results at the laboratory replicate or field replicate level, and
    c. calculating derived variables (such as Total PCBs, Total PAHs, LPAH, HPAH, cPAH, etc.) and/or user defined derived variables,
4. compare your searched and processed data to the selected cleanup criteria and/or user defined cleanup criteria,
5. run predefined statistical analysis based on your selected analysis criteria and statistical parameters,
6. identify potential indicator hazardous substance (PIHS) per PIHS Decision Tree in Appendix H of MyEIM User Manual,
7. calculate background concentration and 95% UCL of the mean per MTCA Statistics Engine,
8. calculate lipid normalized tissue concentrations and TOC normalized sediment concentrations when tissue percent lipid and sediment TOC are reported in EIM,
9. make visually pleasing and informative maps of sampling locations and hits, and
10. compare searched bioassay data to the selected bioassay criteria.

The following pages (interfaces) will be discussed more in depth in the chapter:

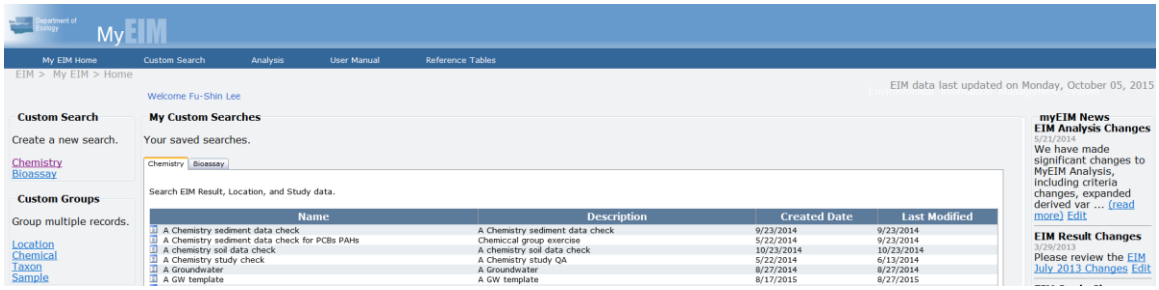
- Home (Portal)
- Search Interface:
    - Chemistry Search
    - Bioassay Search
- Results (Records):
    - Bioassay Data
    - Chemistry Data
- Custom Groups
- EIM Map Viewer (GIS)
- Chemistry Analysis
- Bioassay Analysis
- MTCA Statistics

About this Manual

This manual provides insight on using MyEIM to search, view, map, and compare your data to known standards - as well as perform many other functions using EIM data. Throughout this manual you will find exercises and labs to help you use MyEIM to its full potential. Exercises walk you through the steps needed to complete a task. Labs take you through real-world scenarios using MyEIM, testing your knowledge and highlighting the features covered in this manual.

ACCESSING MYEIM

MyEIM is available to everyone. However, there are two separate website addresses for Ecology staff and the public. This is for security purposes. Find the links below for intranet and internet access.



MyEIM Home Page

Before accessing MyEIM, review the user requirements section.

User Requirements

MyEIM is best used with Internet Explorer 7-11, although other browsers might be compatible. Pop-up blockers can prevent MyEIM from accessing outside resources or from downloading data. We recommend turning off your pop-up blocker when using MyEIM.

Intranet (Ecology Staff) Access to MyEIM

Ecology staff are automatically logged in to MyEIM via this link: http://myeim. Browser settings can prohibit automatic recognition of your identity. If you are unable to access MyEIM, see Appendix B for troubleshooting. We recommend using the Intranet version if possible, but if you must access MyEIM via SecureAccess Washington, register using your work email so that information such as saved queries will be synced with your internal account.

Internet (Public) Access to MyEIM

Public users must use SecureAccess Washington (SAW), the State's security gateway, to access MyEIM: https://secureaccess.wa.gov/ecy/myeim. See Appendix A for information on registering for and accessing MyEIM via SAW.

RESOURCES

Additional resources can be found at MyEIM portal page. This may include news announcements such as MyEIM training events, MyEIM application updates including new and enhanced features, focused sheets as well as an updated manual with associated video tutorials.

Technical Support

Contact MyEIM technical support by using our online form at https://fortress.wa.gov/ecy/eimreporting/Help/Contact.aspx

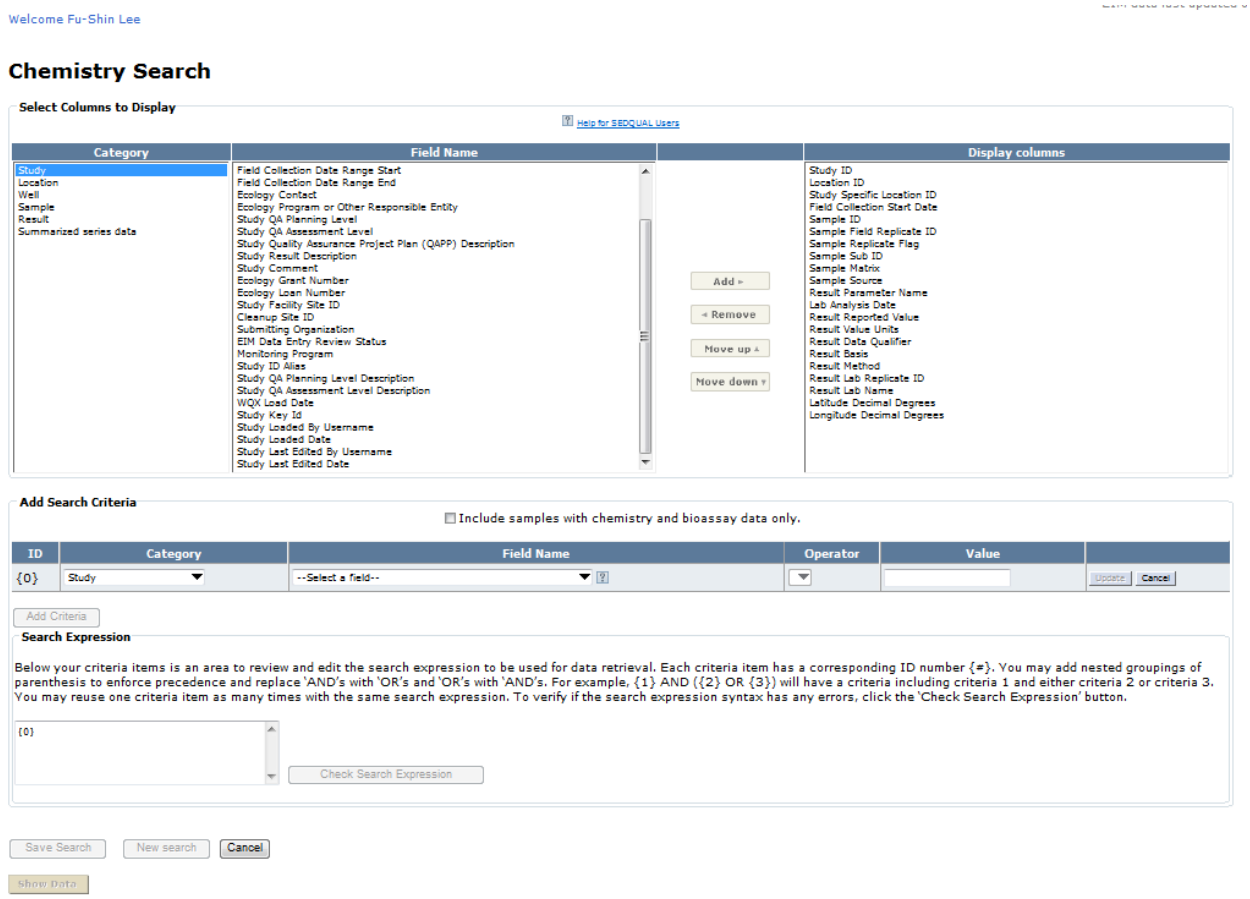
or

Contact Person	Telephone	Email
Fu-Shin Lee	(360) 407-6237	fu-shin.lee@ecy.wa.gov

Chapter 1: Search Page

Select columns of data to be displayed, set criteria, save a search and submit a search.

OVERVIEW

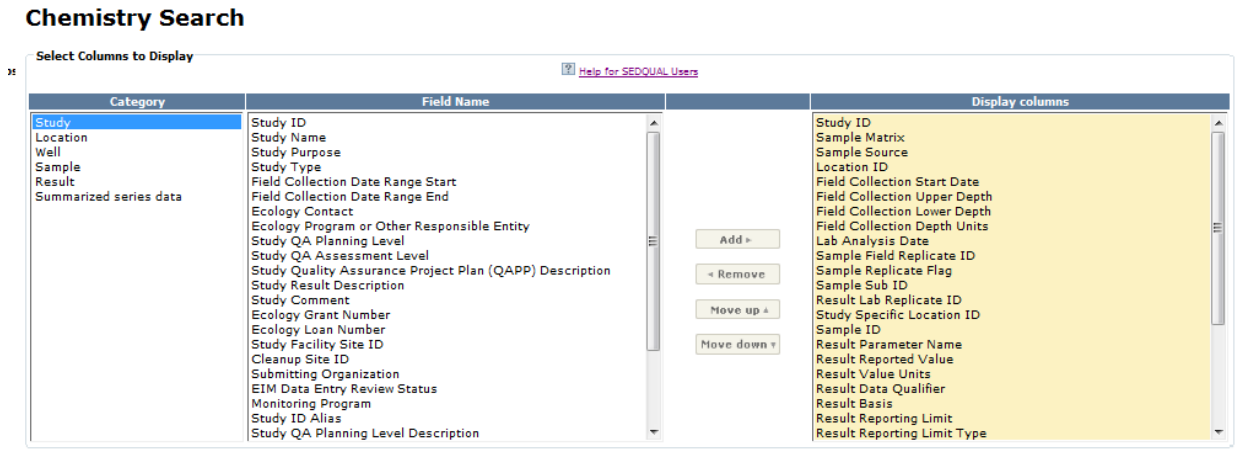


The Search Interface

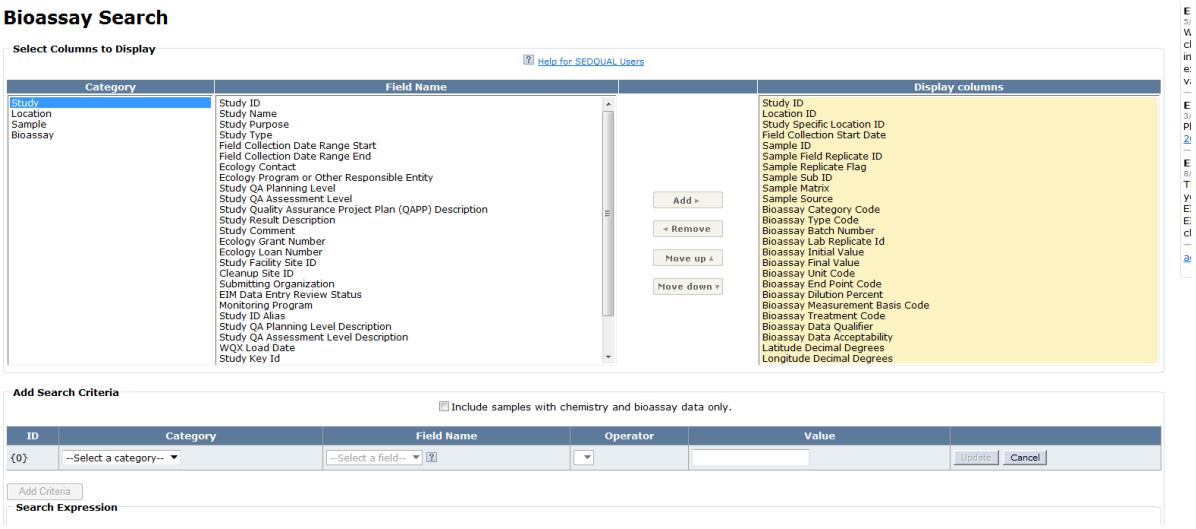
The Search page allows you to select from a list of available EIM fields to be displayed for viewing from the Results page and to be used as search criteria. The search is edited and saved on the Search page. This chapter will guide you on creating a new search for retrieving the data of your interest and saving the created search.

STEP 1. SELECT COLUMNS TO DISPLAY

The first step on searching for EIM data is to select what EIM fields of data you want to display in Display Columns. When creating a new search, we have provided a default set of columns for chemistry and bioassay search in Custom Search, and quick start chemistry and bioassay searches in Search Templates. You may modify with your own set of EIM columns.



MyEIM Chemistry Search Page



MyEIM Bioassay Search Page

About Display Columns

Display Columns are EIM field names to be displayed as headers in the Results page and the downloaded spreadsheet files. 'Help for SEDQUAL users' will provide a crosswalk between SEDQUAL terms and EIM terms.

Adding Display Columns

You may add fields to the 'Display Columns' list by selecting one or more fields from the 'Field Name' list then click the 'Add' button. The 'Field Name' lists are grouped by categories.

Removing Display Columns

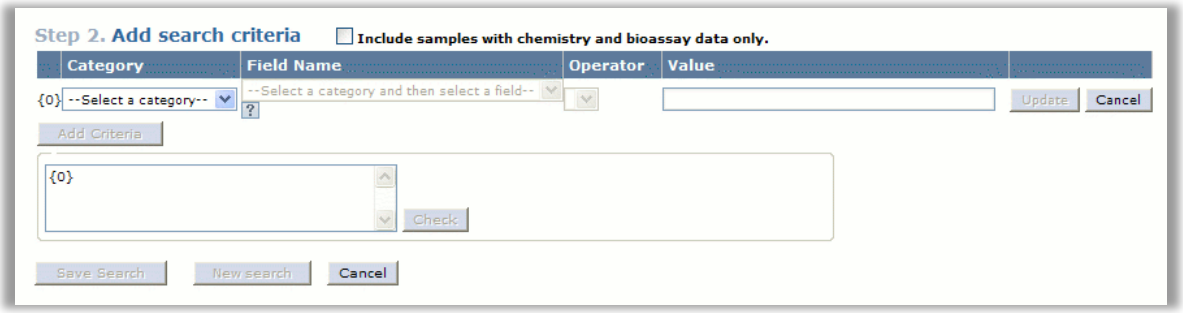
You may remove fields from the 'Display Column' list by selecting one or more fields from the 'Display Columns' list then click the 'Remove' button.

Ordering Display Columns

You may modify the sequence of the resulting headers by selecting one or more fields from the 'Display Columns' list then click 'Move Up' or 'Move Down'.

STEP 2. ADD SEARCH CRITERIA

Once we have your EIM fields of interest arranged in the right order in 'Display Columns' set, the next step is to add the search criteria of interest.



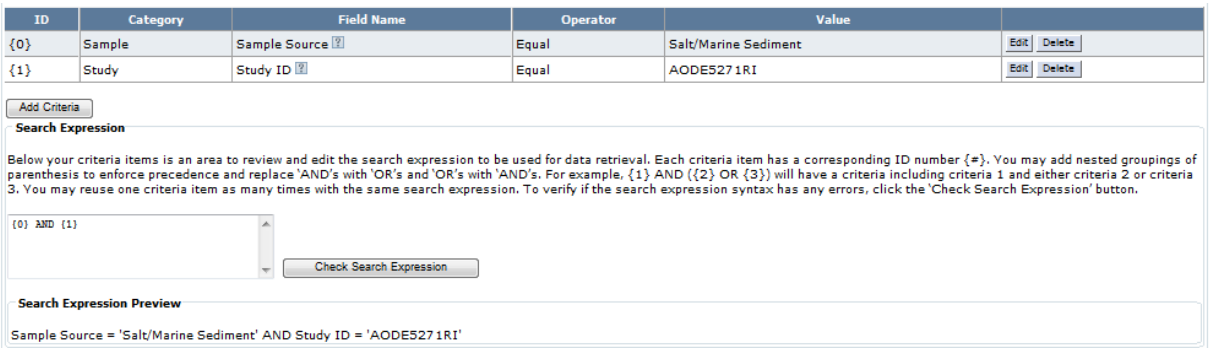
'Include Samples with Chemistry and Bioassay Data Only' Option

This option when checked will retrieve data that only includes synoptic data.

Selecting a Category/Field/Operator/Value as one criteria item

Select a ‘Category’ then a ‘Field Name’ of interest. Once a ‘Field Name’ is selected, a help icon will be available and when pressed will provide the EIM term help information of the selected ‘Field Name’. The ‘Operator’ provides a list of comparison values based on your ‘Field Name’ selection and does vary for each field selected. ‘Value’ is where you would enter or select the criteria’s value. Click ‘Update’ to add the criteria item or click ‘Cancel’ to discard the criteria item. You may click ‘Delete’ to remove the criteria item or click ‘Edit’ to edit an existing criteria item.

Setting Precedence and using AND/OR Keywords



Below your criteria items is an area to review and edit the search expression to be used for data retrieval. Each criteria item has a corresponding number {#}. You may add nested groupings of parenthesis to enforce precedence and replace ‘AND’s with ‘OR’s and ‘OR’s with ‘AND’s. For example, {1} AND ({2} OR {3}) will have a criteria including criteria 1 and either criteria 2 or criteria 3. To verify if the search expression syntax has any errors, click the ‘Check Search Expression’ button.

STEP 3. SEARCH OPTIONS

Once the criteria have been supplied, you now can perform the following options.

Saving ‘My Custom Search’

To save your search, click the ‘Save Search’ button. A dialog box will appear prompting you to enter a name of the search and optionally a description of the search. You may click ‘Cancel’ to discard saving the search. Click ‘Save Search’ from the dialog box will save your search for later retrieval and will list your search in the ‘My Custom Search’ section of the MyEIM Home page. A message will appear stating your search has been saved successfully with the name and description.

Discarding Changes

To cancel any changes made to an existing search and/or to simply close the Search page and be redirected to MyEIM Home page, click the ‘Cancel’ button.

Perform a New Search

To perform a new search using the default ‘Display Columns’ with no criteria for Chemistry and Bioassay custom search , click the ‘New Search’ button.

Submit a Search

To submit a search which will retrieve data based on your ‘Display Columns’ and criteria selection, click the ‘Show Data’ button to view the results of your interest in the Results page.

Exercise 3:

Create, save and submit a new Chemistry search for Synoptic Chemistry and Bioassay Locations

(1) From MyEIM Home, select the 'Chemistry Study QA' in Search Templates. Clicking on "Save as" will bring you to the Search page.

(2) Within the 'Display Columns' list, select the 'Study Type' field and while holding onto the 'Shift' key on your keyboard, select the 'Study Name' field then click the 'Remove' button.

(3) Within the 'Category' list, select 'Location' then from the 'Field Name' list select 'Location ID' and while holding the control key on your keyboard select 'Study Specific Location ID' then click the 'Add' button.

(4) Within the 'Display Columns' list, select 'Location ID' and click the 'Move down' button until it is the last field listed.

(5) Remove 'Field Collection Date Range Start'. Add 'Field Collection Start Date' under Sample. Move 'Field Collection Start Date' above 'Study Specific Location ID'.

(6) Check the box 'Include samples with chemistry and bioassay data only'.

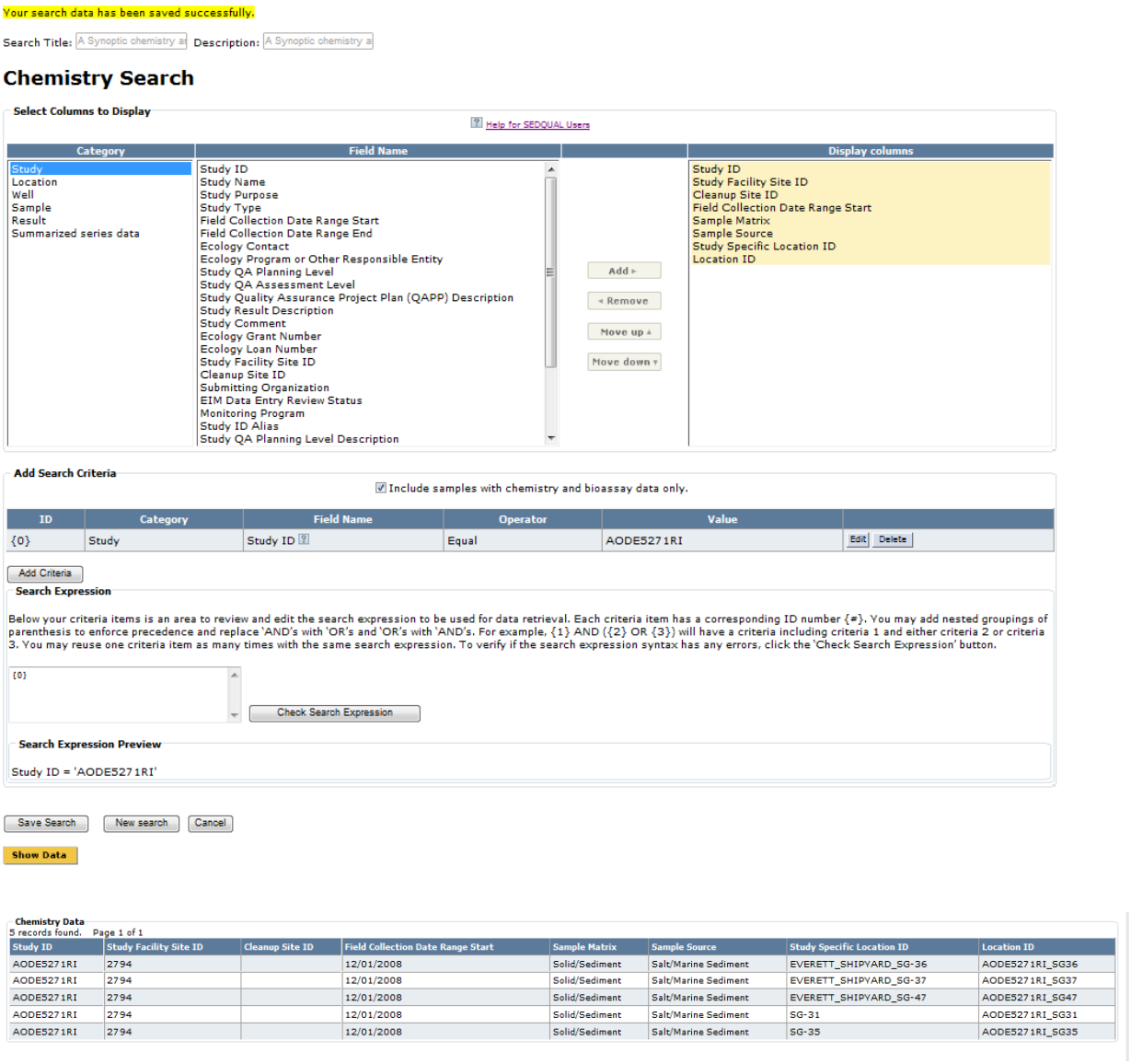
(7) Click on 'Save Search' and type 'A synoptic chemistry and bioassay location' in Search Name, and click on "Save Search". The yellow highlighted 'Your search data has been saved successfully' will be shown close to the top of the Search page.

(8) Click the 'Show Data' button. You will be redirected to the Results page with 5 records displayed per the selected 'Display Columns' and search criteria. To return to the MyEIM Home, click on the 'My EIM Home' or 'My EIM' link.

(9) 'A synoptic chemistry and bioassay location' will be shown under 'My Custom Searches' of MyEIM Home page.

(10) Select 'synoptic chemistry and bioassay location' in My Custom Searches and clicking on "Save As" will bring you to the Search page.

(11) Uncheck "Include samples with chemistry and bioassay data only".



(1) Clicking on 'Show Data' will bring you back to the results page with 268 records.

This completes Exercise 1.

LAB 1: CREATE A CHEMISTRY SEARCH WITH YOUR DATA OF INTEREST

Select your own ‘Display Columns’ and criteria of interest for a new chemistry search. Bioassay searches will be covered in Chapter 6: bioassay analysis.

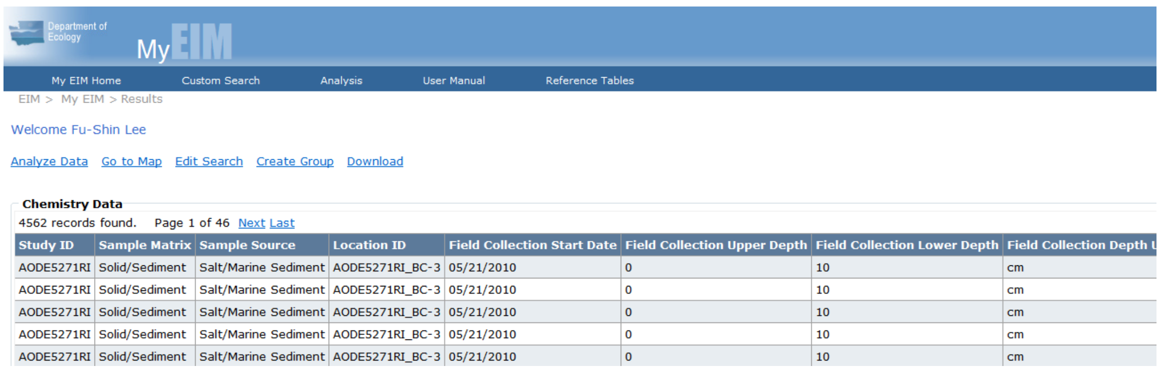
Refer to exercise 1 as a helpful resource. If your search attempts to return a high volume of records, you may receive a message stating that it has exceeded the record limit and to further narrow your search criteria.

If you feel you have advanced, try adding many criteria items in order to modify the search expression with parenthesis for precedence and using the ‘AND/OR’ keywords.

Chapter 2: Results Page

View and download Chemistry or bioassay data from the selected search.

OVERVIEW

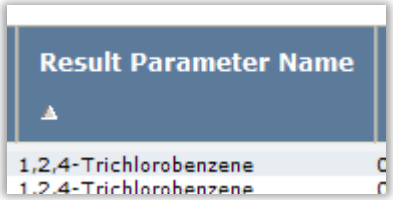


The Results Page

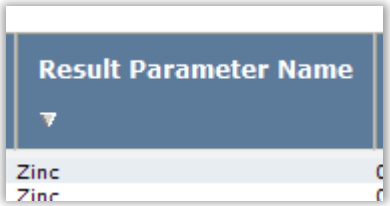
The Results page displays a table of EIM records based on the ‘Display Columns’ and criteria submitted from the Search interface. You may at times need to scroll up/down/left/right for viewing searches containing many records and/or many display columns.

SORTING

To sort by a particular display column, click on the desired display column's text. A triangle icon will appear indicating that the selected display column is sorted in ascending order. To sort in descending order, click on the desired display column's text where the triangle exists and an upside down triangle icon will appear indicating that the column is sorted in descending order. You can toggle between ascending and descending order by repeatedly clicking on the desired display column's text which the column is currently sorted by.



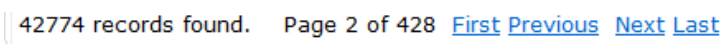
Sorted Ascending



Sorted Descending

NAVIGATING

If a search returns over 100 records, navigation links will appear. Records are displayed 100 records at a time per page. To navigate between pages, click on the "Next", "Previous", "First" and "Last" navigation links.



RECORDS OPTIONS

With the table of records, you can perform the following options.

Download

Click on the 'Download' link to export the table of records as a comma separated values file (CSV file) which can be saved and opened as csv (Comma delimited) or xlxs (Excel Workbook) files by Microsoft spreadsheet program. In an event the amount of records are high, the CSV file may be compressed as an archived file (ZIP file) which on average reduces the size ten times the original size.

Create Group

Click on 'Create Group' to create a custom group for 'Location Group' and/or 'Sample Group' based on the selected criteria and display EIM fields. Provide a 'Name' and 'Description'. Custom Groups is covered in great detail in the Home page chapter.

Edit Search

Click on "Edit Search" to return to the Search page which you may further modify and save the current search. The 'Custom Search' link that is located on the top just below the MyEIM banner will also behave as 'Edit Search' from the Results page, however the 'Custom Search' link will bring you a new search from the MyEIM Portal interface.

Go to Map

Click on "Go to Map" to map the associated locations on your searched table of records. The GIS page chapter in this manual covers the GIS page in greater detail.

Analyze Data

Click "Analyze Data" to perform analysis based on your searched table of records. The Analyze Data feature is covered in the chemistry and bioassay analysis chapters of this manual.

Exercise 4:

View, Download and Map Searched EIM Data and Create Location Group

(1) Clicking on Chemistry link under Custom Search of MyEIM Home page will bring you to the Search page with the default 'Display Columns' and add one criteria item where 'User Study ID' 'Equals' 'PSDDA_95', then click 'Show Data' to be redirected to the Results page.

(2) From the records interface, scroll to the right then back to the left using the browser's scroll bars. Scroll down then up using the browser's scroll bars. If your mouse is equipped with a scrollable wheel, click on the table of records and scroll the mouse wheel down then up. If you do not have a mouse with a scrollable wheel, scroll all the way to the right using the browser scroll bar. There will be another scrollbar to scroll the table of records.

(3) Click the "Result Parameter Name" display column's text to sort in ascending order.

(4) Click the "Next" navigation link. Once you are on page 2, click the "Last" navigation link. Once you are on the last page, click the "Previous" navigation link.

(5) Click the "Download" link to export the table of records from the records interface as a CSV file.

(6) Click the 'Go to Map' link. You will be redirected to the GIS page with locations highlighted on the map based on your table of records.

(7) To return to the Search page, click on the "Go Back" link located in the top right dark blue navigation bar of the GIS page. Create location group by clicking on 'Create Group' entered PSDDA_95 to the Name, selecting Location Group and Click on 'Save'. Click "My EIM Home" link to return to MyEIM Home page.

This completes Exercise 2.

LAB 2: VIEW, SORT AND DOWNLOAD RECORDS A SEARCH WITH YOUR DATA OF INTEREST

Select the default ‘Display Columns’ and your criteria of interest for a new chemistry search that will return at least 400 records.

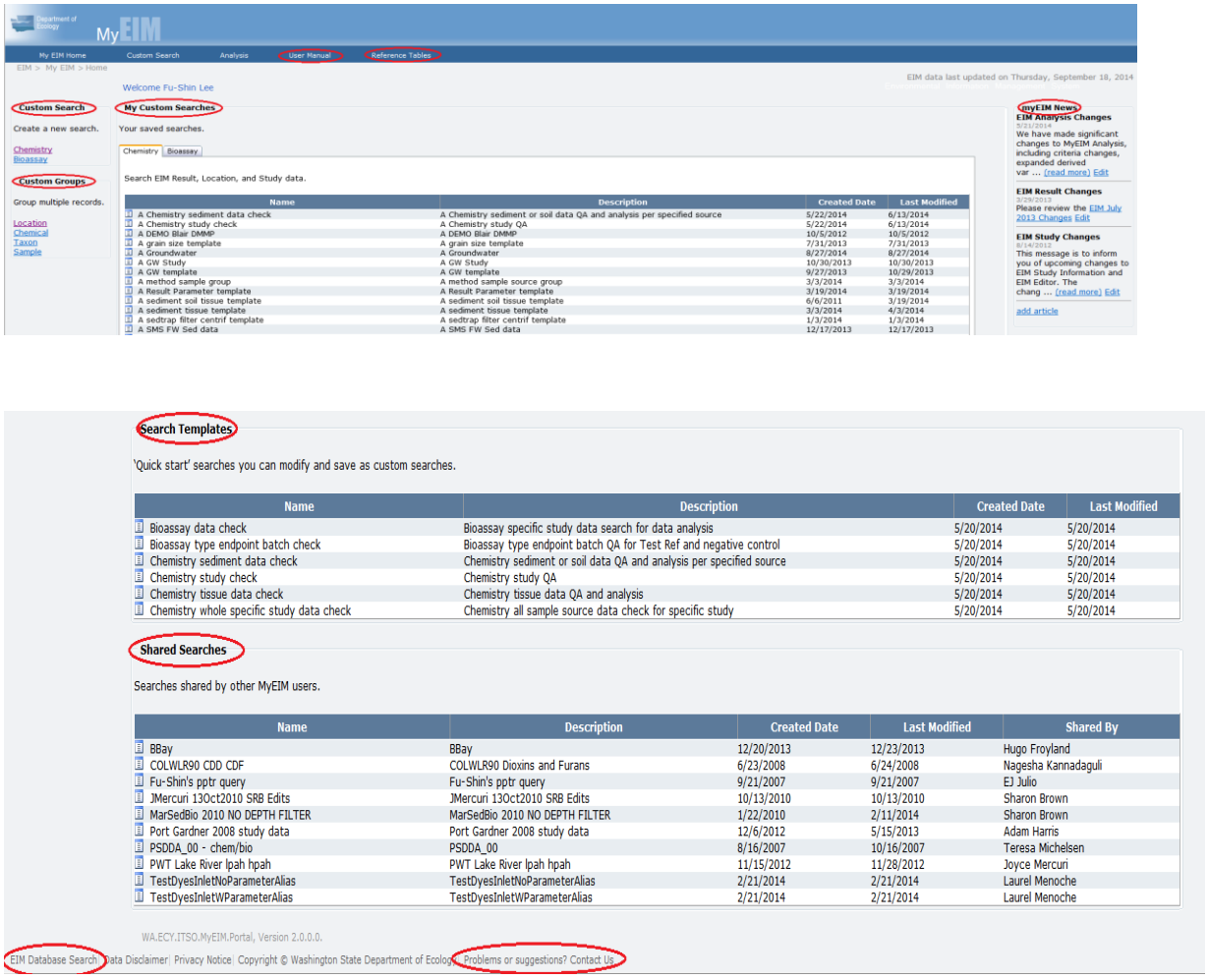
From the records interface, view the table of records which was based on your search by using the browser’s scroll bars and navigation links. Download your data.

Create a ‘Location Group’ and ‘Sample Group’ from the Results page. ‘Custom Groups’, ‘Analyze Data’ and ‘GIS’ is covered in great detail in their respective chapters.

Chapter 3: Home Page

The home page of MyEIM allows you to manage searches and custom groups, and access MyEIM/EIM news items, EIM Reference Table, EIM Database Search as well as a 'Contact Us' feedback form.

OVERVIEW

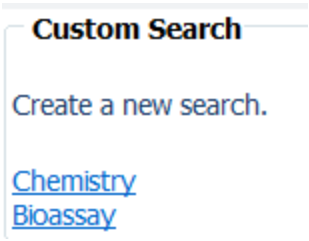


MyEIM Home Page

MyEIM home page has the following key components to be entailed in the following sections:

- Custom Search
- Custom Groups
- My Custom Search
- Search Templates
- Shared Searches
- MyEIM / EIM News
- Additional Resources

CUSTOM SEARCH



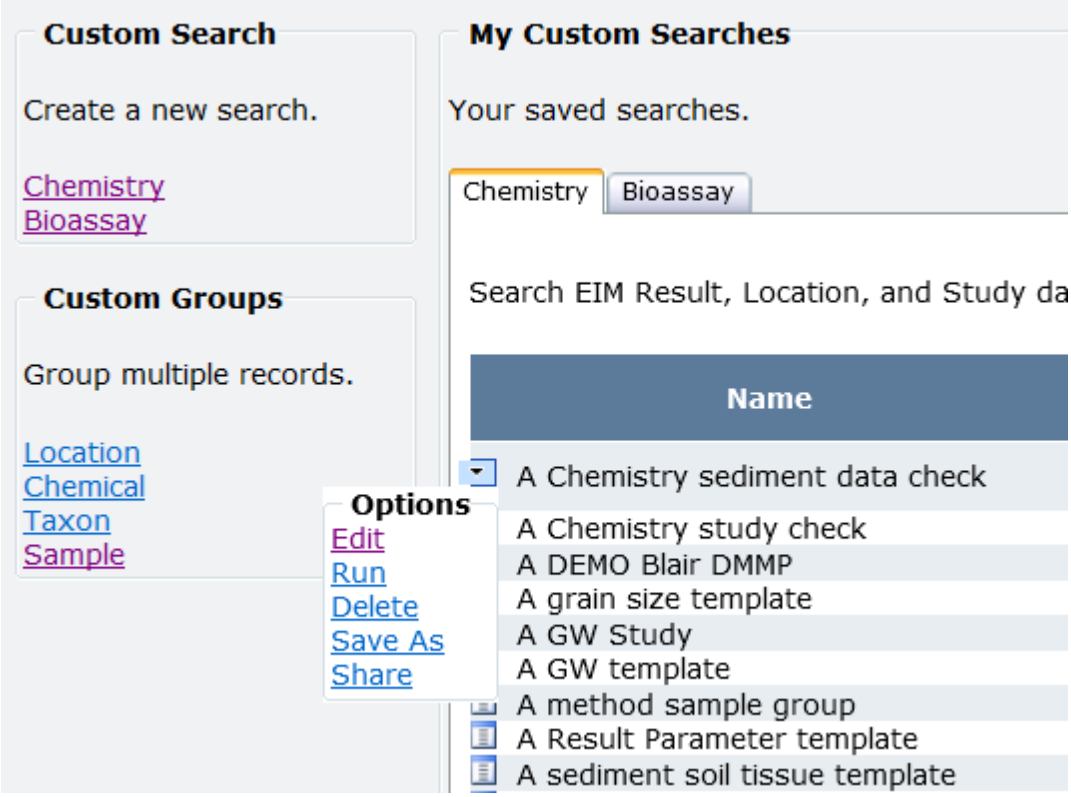
The "Custom Search" section allows you to create and save a new search based on the selected links. Currently, you can create a new chemistry and bioassay search. In the future, there will be other types of searches from this section.

CUSTOM GROUPS

The Custom Groups Section allows you to create a location or chemical or taxon or sample group of interest based on the selected link.

MY CUSTOM SEARCHES

The 'My Custom Searches' section lists your previously saved . searches. Click on located at the left side of the search name to access the following options and their action explained in the following table.

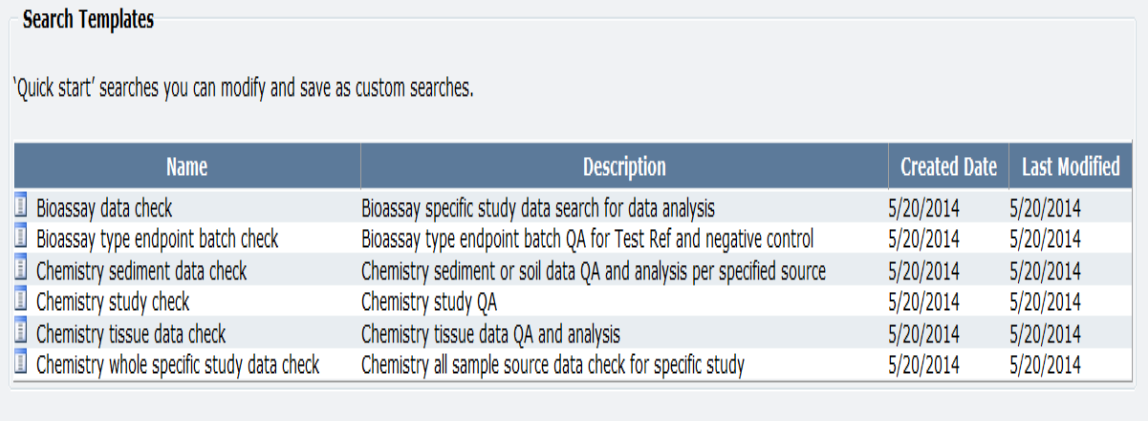


Option	Action
Edit	Redirects the selected search to the Search page.
Run	Redirects the selected search to the Results page.

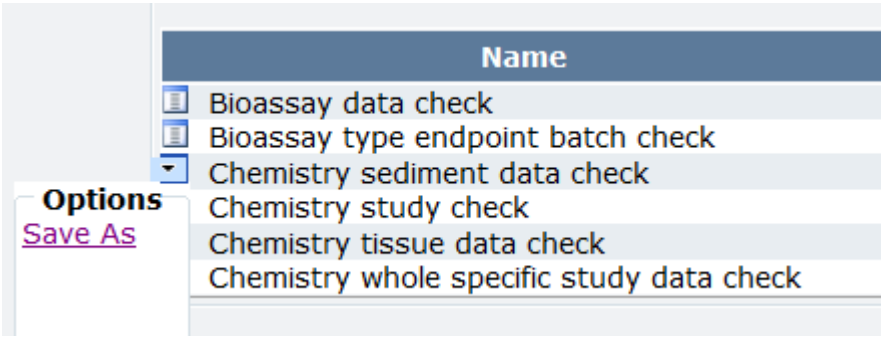
Option	Action
Delete	Redirects the selected search to the Search page in read-only mode with a prompt to confirm deletion.
Save As	Redirects the selected search into the Search page which the search may be modified if desired and provides a way to save the selected search with a different name to be provided.
Share	Sends a duplicate copy of the selected search to another MyEIM user to be selected from a list of all available MyEIM users. The MyEIM user recipient will receive the search listed in their 'Shared Searches' section of MyEIM Home page.

SEARCH TEMPLATES

Search templates are predefined searches which provide 'Quick Start' searches to all MyEIM users, and the users can modify and save the modified search in 'My Custom Searches' section of MyEIM Home page.



Click on located at the left side of the search name to access the ‘Save As’ option.



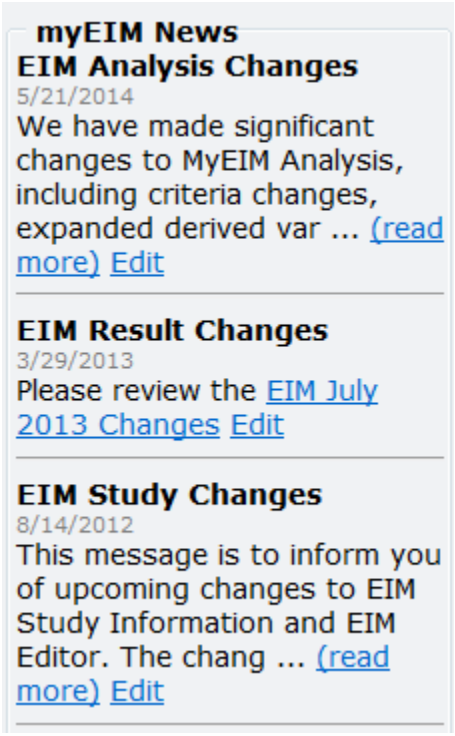
Option	Action
Save As	Redirects the selected search into the search interface which the search may be modified if desired and provides a way to save the selected search with a different name to be provided. Once saved, the search will be listed in the “My Custom Searches” section.

SHARED SEARCHES

Acts as an inbox of searches sent from other MyEIM users. Click on  located at the left side of the search name to select the 'Save As' option to access the shared search or to select the 'Delete' option to delete the shared search.

Option	Action
Save As	Redirects the selected search into the Search page which the search may be modified if desired and provides a way to save the selected search with a different name to be provided by the user. Once saved, the search will be listed in the "My Custom Search" section.
Delete	Redirects the selected search into the Search page in read-only mode with a prompt to confirm deletion.

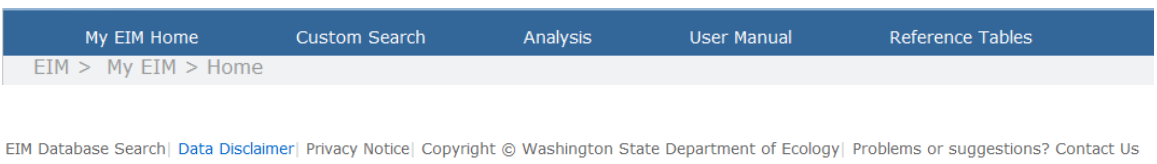
MYEIM / EIM NEWS



The MyEIM / EIM News section may contain news announcements such as MyEIM training events, MyEIM application updates including new and enhanced features as well as an updated manual with associated video tutorials, and EIM update news. Click on an MyEIM / EIM news item to access the detailed news article. The MyEIM / EIM news section is administered by the MyEIM / EIM application administrator(s).

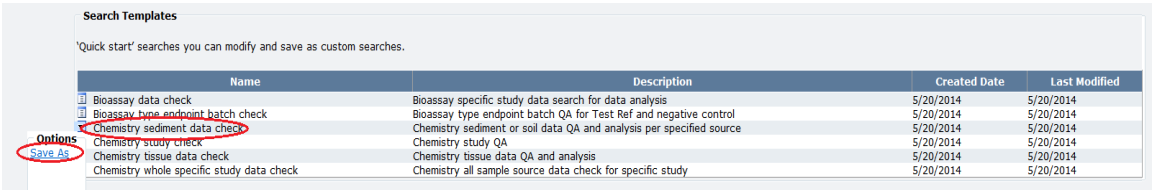
ADDITIONAL RESOURCES

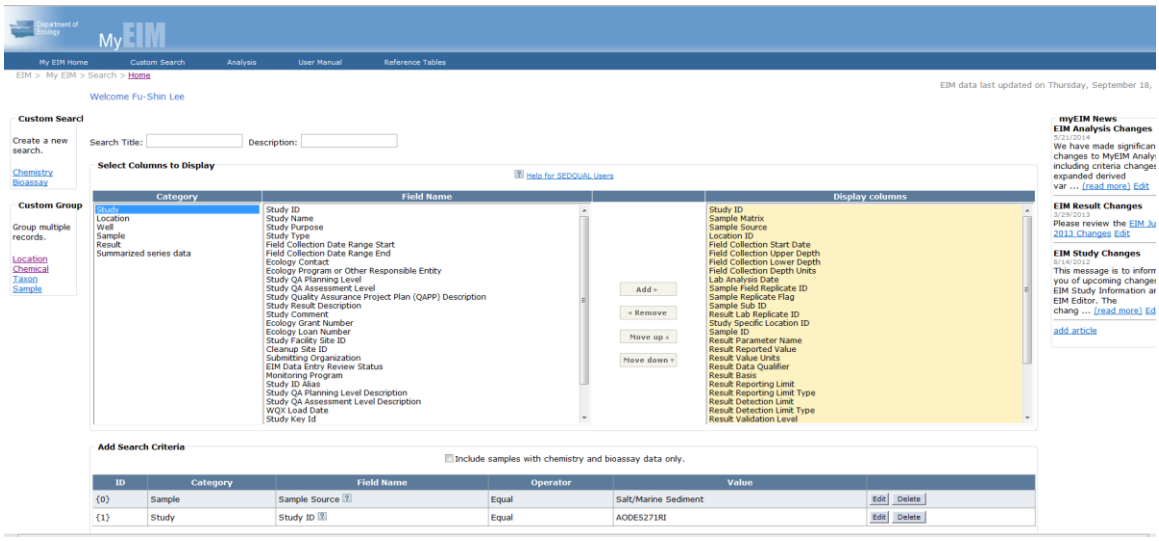
Additional resources linked to MyEIM can be found in the top dark blue navigation bar and the bottom gray footer. A new browser window will open on accessing these links. Additional resources include MyEIM User Manual, EIM Reference Table, EIM Database Search as well as a 'Contact Us' feedback form.



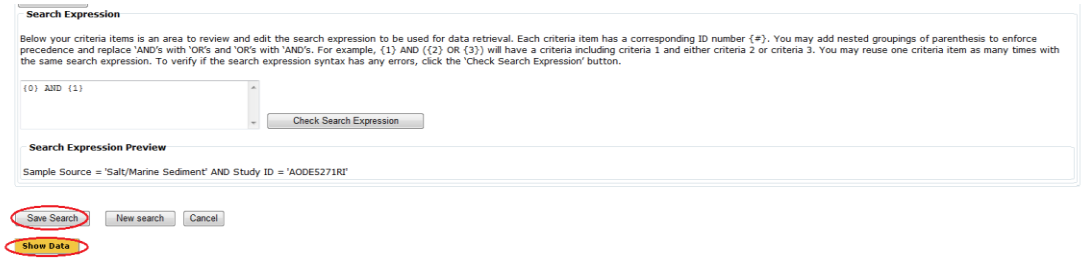
Exercise 1: Use a Search Template then Share Your Search

(1) From MyEIM Portal, Search Templates section, click on  on the left next to the search named “Chemistry sediment data check” and select the ‘Save As’ option. You will be redirected to the chemistry search page.

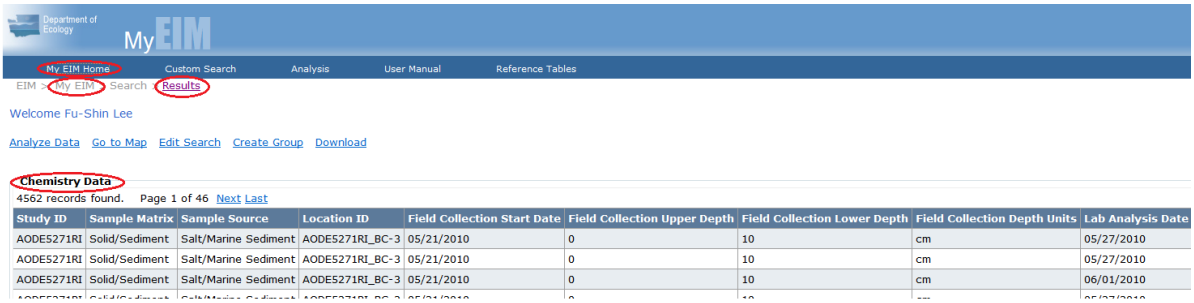




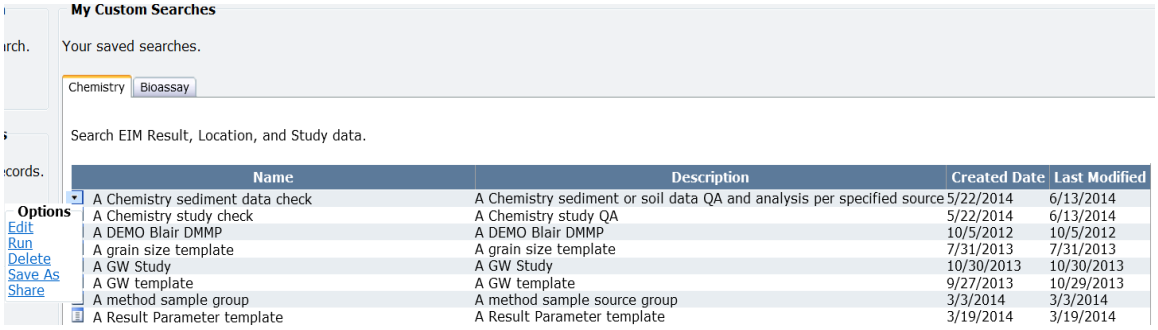
(2) Click the ‘Save Search’ button. From the dialog box, type “A Chemistry Sediment Data Check” in the ‘Search Title’ box then click the ‘Save Search’ button.



(3) Click the ‘Show Data’ button. You will be redirected to the results page for Chemistry Data. Once the table of records are displayed onto the records interface, click the “My EIM” link from the breadcrumb navigation (EIM > My EIM >) located just above the “Welcome: [Your Name]” greeting. This “My EIM” link behaves just the same as if you’d click on the “My EIM Home” link from the top dark blue navigation bar.



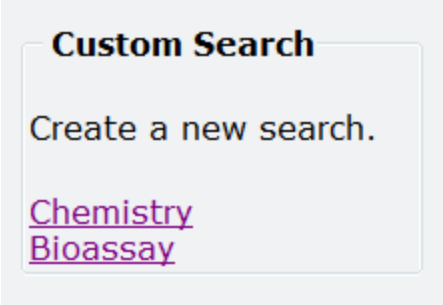
(4) “A Chemistry Sediment Data Check” should now be listed in the ‘My Custom Searches’ section. Click on “A Chemistry Sediment Data Check” and select the ‘Share’ option. A dialog box will appear and you will be prompted to select a MyEIM user from the list. Select a MyEIM user then click the “Share” button.



(5) Your MyEIM user recipient should now be able to have a copy of your search listed in their ‘Shared Searches’ section. This complete exercise 1.

LAB 1: CREATE A NEW CHEMISTRY SEARCH WITH CUSTOM SEARCH, SHARE THE SAVED SEARCH, AND DELETE THE SHARED SEARCH

Clicking Chemistry in Custom Search of MyEIM home page will direct you to the Chemistry Search page.

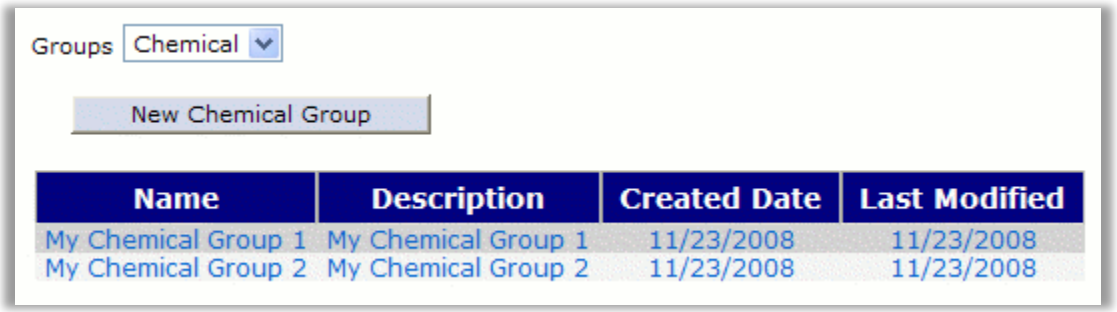


Select your own 'Display Columns' and criteria of interest for a new chemistry search. Click 'Show Data' to verify that your search has records. Click on 'Save Search' to save your search. Once saved, you'll find your saved search under my Custom Searches of MyEIM home page. Share your search to others.

Once you receive a shared search under the Shared Searches of MyEIM home page, click the 'Save As' option to be redirected to the search interface to view the display columns and search criteria. Then click 'Show Data' to view the results on the Results page. After viewing the results, go back to MyEIM Portal and delete the shared search.

CUSTOM GROUPS

Custom groups allows you to group multiple locations, samples, taxons or chemicals as one criteria item. Click on one of these four custom groups from MyEIM home or search pages to be redirected to the custom groups list interface.



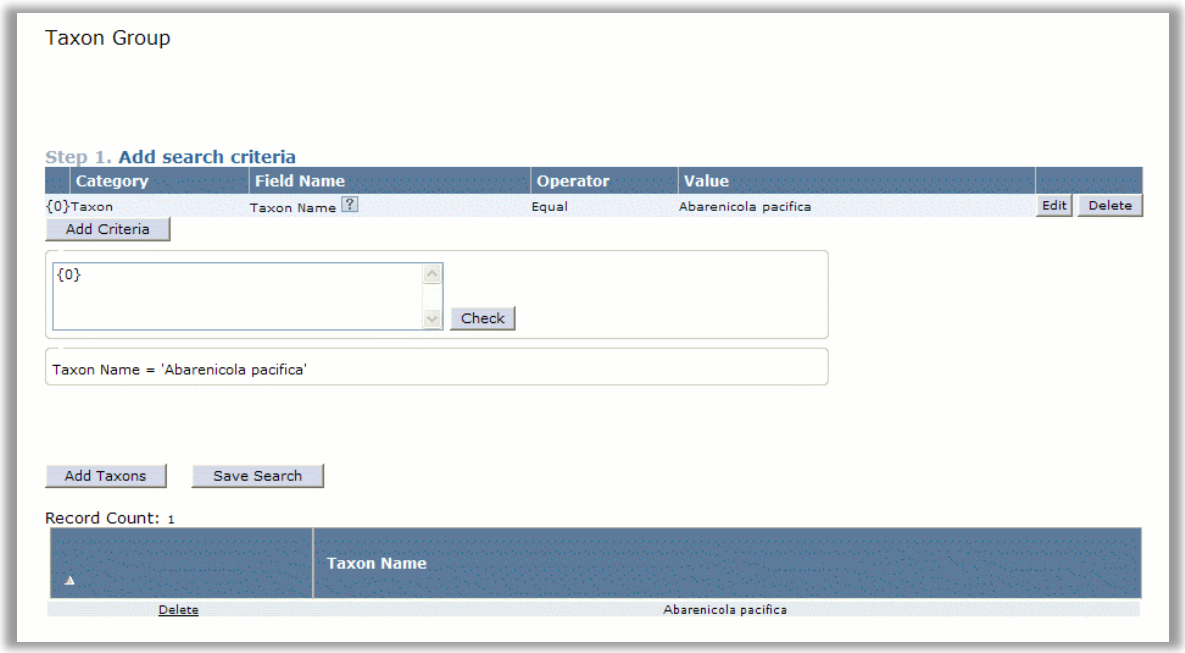
MyEIM Custom Groups List Interface (Chemical Groups shown)

The custom groups list interface lists previously saved custom groups. If no custom groups exist, you will see the message "No searches/groups are available".

From this interface, you may toggle between the four custom groups by selecting the desired custom group from the 'Custom Groups' select box. You can create a new custom group by clicking on the associated "New Group" button which you will be redirected to the corresponding custom groups interface.

From the custom groups list interface, click on the custom group's name to access the following options menu.

Option	Action
Edit	Redirects the selected search into the custom groups interface.
Delete	Redirects the selected search into the custom groups interface in read-only mode with a prompt to confirm deletion.
Save As	Redirects the selected custom group into the custom groups interface which the custom group may be modified if desired and provides a way to save the selected custom group with a different name to be provided.
Share	Sends a duplicate copy of the selected custom group to another MyEIM user to be selected from a list of all available MyEIM users. The MyEIM user recipient will receive the custom group listed in their custom groups list interface.



MyEIM Custom Groups Interface (Taxon Group shown)

The custom groups interface has the same ‘Add Search Criteria’ step found in the search interface. The ‘Back to Groups List’ button simply discard any changes to a custom group.

The associated ‘Append’ button will return a table of records with data related to the selected custom group. The ‘Save Search’ button will save the table of records as a custom group by providing a name and description.

The “Record Count” displays the total amount of records. Each record from the table of records can be deleted. Each custom group may have additional buttons in the interface. After appending records the first time, you may modify the criteria section and append data based on the modified criteria. The table of records will not be overwritten instead data will be appended.

Location Group

There are three ways to create a Location Group.

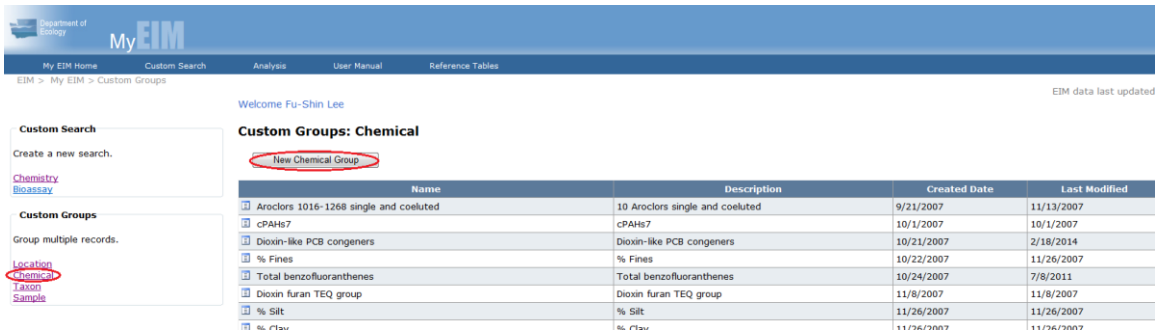
1. Create Location Group in the Results page: You can perform a search in the search page then from the results page, click the ‘Create Group’ link and check the ‘Location Group’ option after providing the name and description. This will create a group of locations based on your search criteria.

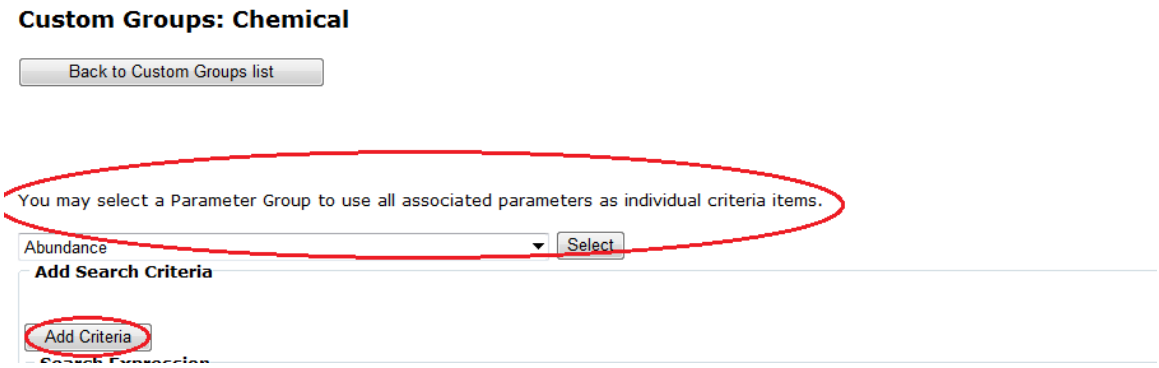
2. Create New Location Group using GIS interface through Location Group in MyEIM home page: Click on ‘Location’ under Custom Groups in MyEIM Home page. You will be redirected to the custom groups list interface for locations. Click the ‘New Location Group using GIS Interface’ button to create a group of locations from the map.

3. Create New Location Group using tabular criteria through Location Group in MyEIM home page: Click on ‘Location’ under Custom Groups in MyEIM Home page. You will be redirected to the custom groups list interface for locations. Click the ‘New Location Group using tabular criteria’ button to create a group of locations from the selected search criteria.

Chemical Group

Click on ‘Chemical’ under Custom Groups in MyEIM Home page. You will be redirected to the custom groups list interface for chemicals. Click the ‘New Chemical Group’ button to be redirected to the custom groups interface. From the custom groups interface, a parameter group select box will be present with the associated “Select” button and individual chemical can be added by clicking on ‘Add Criteria’ under Add Search Criteria. You may select one or more EIM Parameter Group to use all associated parameters within the selected parameter group or / and select individual chemical to be included in your user defined chemical group .





Taxon Group

Click on “Taxon Group” from MyEIM Portal. You will be redirected to the custom groups list interface for taxons. Click the “New Taxon Group” button to be redirected to the custom groups interface to select your taxons of your interest in your user defined taxon group.

Sample Group

There are two ways to create a ‘Sample Group’. You can perform a search from the search interface then from the records interface, click the ‘Create Group’ link and check the “Sample Group” option when providing the name and description.

This will create a group of sample based on your search criteria. The other way to create a sample group is to click on ‘Sample’ under Custom Groups in MyEIM Home page. You will be redirected to the custom groups list interface for samples.

Click the “New Sample Group” button to be redirected to the custom groups interface to select specific EIM fields of interest to create your user defined sample group

USING A CUSTOM GROUP WITHIN A SEARCH

Once user defined custom groups are created, they become available as search criteria items in the Search page.

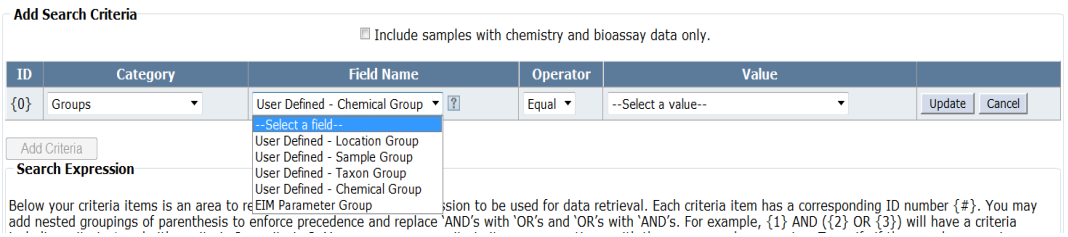
From the ‘Category’ under Add Search Criteria of the Search page, select ‘Groups’.

From the ‘Field Name’ list, select one of the four ‘User Defined’ custom group that you have available.

From ‘Operator’ select ‘Equal’.

From ‘Value’ select your saved user defined custom group then click the ‘Update’ button.

Click the ‘Show Data’ button and you will be redirected to the Results page with the results meeting your criteria which was based on your selected custom group.



Exercise 2: Use a Custom Chemical Group within Your Search

(1) From MyEIM Home page, Custom Groups section, click on the 'Chemical' link. You will be redirected to the custom groups list interface for chemicals.

(2) Click the 'New Chemical Group' button. You will be redirected to the custom groups interface.

(3) From the 'Parameter Group' select box, select 'PCBs'. Click on "Select" button, and Criteria item will be added.

(4) From the 'Parameter Group' select box, select 'PAHs, All'. Click on "Select" button, and Criteria item will be added.

(5) Click the 'Add Chemicals' button. A table of records will appear based on your criteria.

(6) The 'Save Custom Group' button and type "My BCBs PAHs" into the 'Custom Group Name' box then click the 'Save My Chemical Group' button. You will be redirected to the custom groups list interface. You'll see 'My BCBs PAHs' at the bottom of custom chemical group list.

(7) Click the 'My EIM Home' link in the top dark blue navigation bar. This will redirect you to the MyEIM Home page.

(8) Clicking on 'Save As' next to 'A Chemistry sediment data check' under My Custom Searches of MyEIM Home page will redirect you to the Chemistry Search page. Click on 'Add Criteria'. Select 'Groups' from 'Category', from 'Field Name' select 'User Defined - Chemical Group'. From 'Operator' ensure 'Equal' is selected. From 'Value', select 'My BCBs PAHs' from the list then click the 'Update' button.

(9) Click the 'Save Search' button in the Search page, Edit the Search Tile as "A Chemistry sediment data check for PCBs PAHs", and Description as 'Chemical group exercise', then click Save Search to save the edited search.

(10) Click the 'Show Data' button to view the searched results based on the selected search criteria for Sample Source, Study ID and user defined chemical group. This completes exercise 2. To return to the MyEIM Home, click on the "My EIM Home" link.

LAB 2: CREATE CUSTOM GROUPS AND CREATE SEARCHES WITH IT

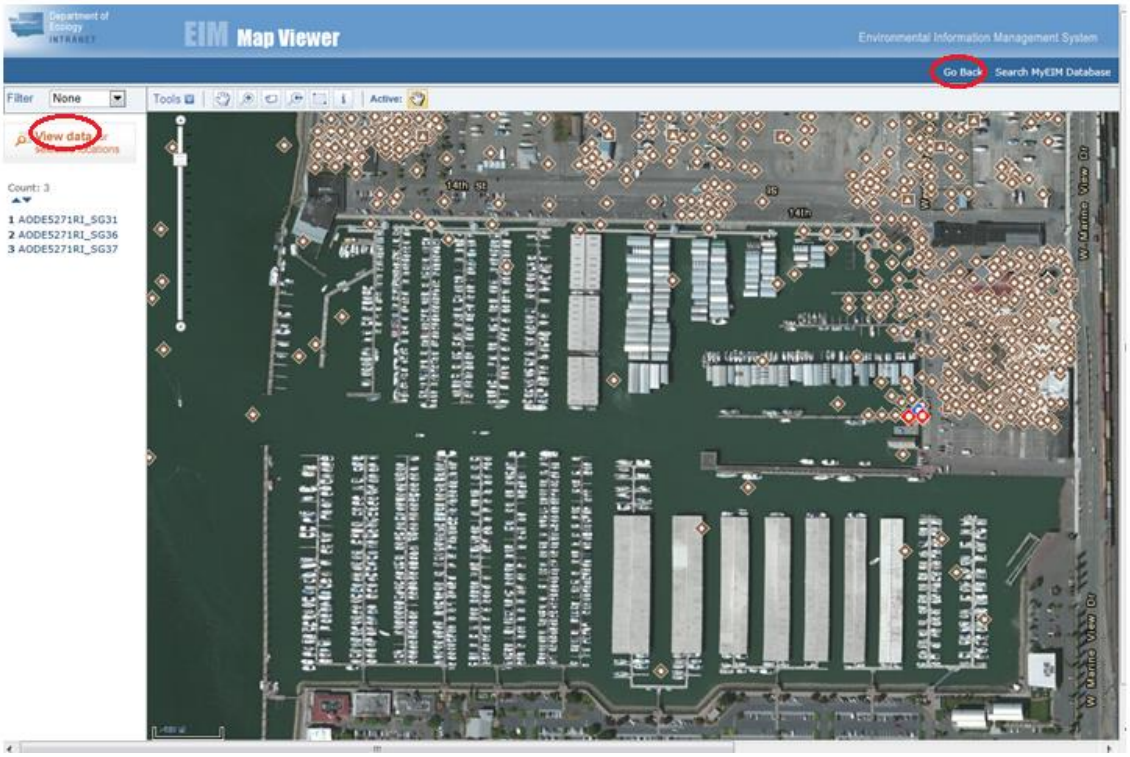
Create a location tabular group, chemical group, taxon group and sample group. Use these groups in a new chemistry search and view the results.

Try adding more than one custom group with a search.

Chapter 4: GIS Page

Map the EIM searched or analyzed results, and create the user defined location group.

OVERVIEW



The GIS Page (also known as the EIM Map Viewer)

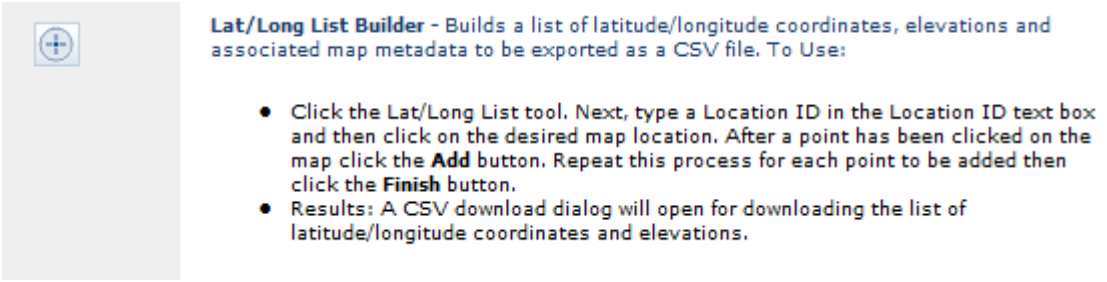
The EIM Map Viewer page allows you to view EIM searched or analyzed data on the map or create s user defined location group.

To access the Map Viewer, perform one of the following tasks described below.

Map MyEIM searched results onto the map from a search

From the Results page, click on "Go to Map". This will redirect you to the GIS page with your searched results with coordinate information on the map. The highlighted blue dots on the map represent your search results associated locations. To return to the results interface, click either the 'Go Back' link located on the top right dark blue navigation bar or the 'View Data' button located at the top left of the Map Viewer. You may modify your locations by add/remove additional locations from the map by zooming to the location area of interest, selecting 'Add to selection' or 'Remove from selection' under Action after selecting  Box Select or  Polygon Select from the 'Tools' dropdown list.

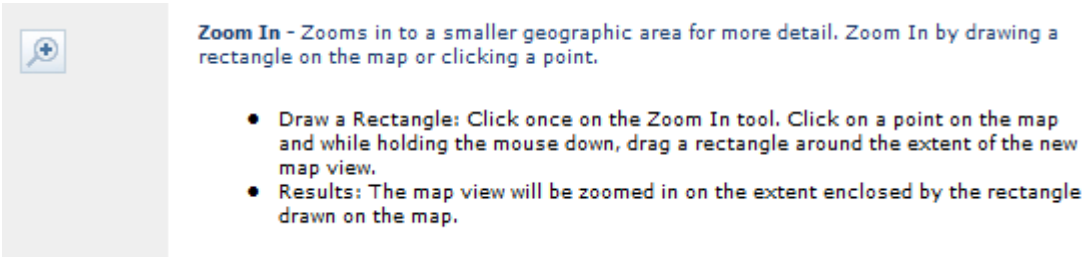
Clicking on 'View Data' will redirect you to the results interface, another message will remind you that the search result is updated and displayed based on station record(s) you have chosen from the GIS application. You may save the modified location group by clicking on 'Create Group'. Providing Name, selecting location group, and clicking 'Save' will redirect you back to the Results interface with the yellow highlighted message to tell inform you that your group record has been save successfully.

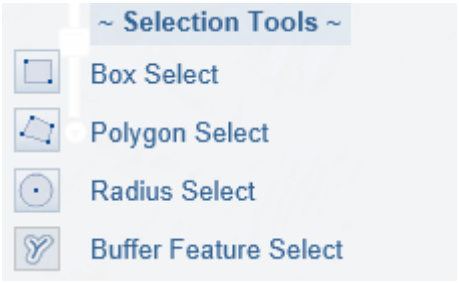


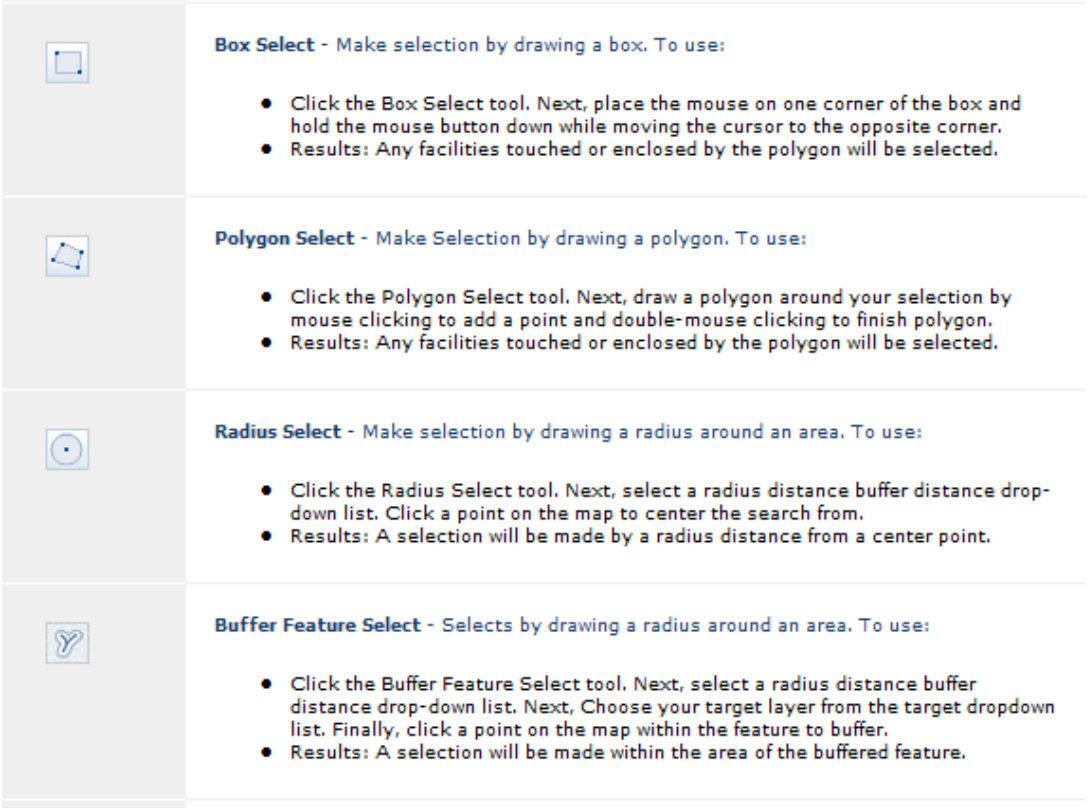
Create a location group using the GIS interface

From MyEIM Home page, click the ‘Location’ link from the Custom Groups section. Click the ‘New Location Group using GIS interface’ button. The GIS interface will show in full Washington state zoom. Zoom into an area of interest. Select locations on the map using one of the selection tools in the ‘Tools’ dropdown list located on the top left grey bar of the GIS page shown below. If you don’t know how to use the selection tools, follow the instruction in the ‘Help’ dropdown located on the top right grey bar of the GIS page for each selection tool as shown below.

Once your location group is created, click the ‘View Data’ button. By clicking the ‘View Data’ button, you will be redirected to the ‘Custom Groups’ page for locations. The ‘Custom Groups’ page will display a table of records of your selected locations. This is exactly the same interface used to create a location group using tabular criteria. You can now delete individual locations from the table of records if desired. Click the ‘Save Custom Group’ button and provide a ‘Name’ and optionally a ‘Description’ then click the ‘Save My Location Group’. Your location group is now available to be used as a search criteria item. Refer to the exercise in the Home page chapter on using your location group within a search.







Box Select - Make selection by drawing a box. To use:

- Click the Box Select tool. Next, place the mouse on one corner of the box and hold the mouse button down while moving the cursor to the opposite corner.
- Results: Any facilities touched or enclosed by the polygon will be selected.

Polygon Select - Make Selection by drawing a polygon. To use:

- Click the Polygon Select tool. Next, draw a polygon around your selection by mouse clicking to add a point and double-mouse clicking to finish polygon.
- Results: Any facilities touched or enclosed by the polygon will be selected.

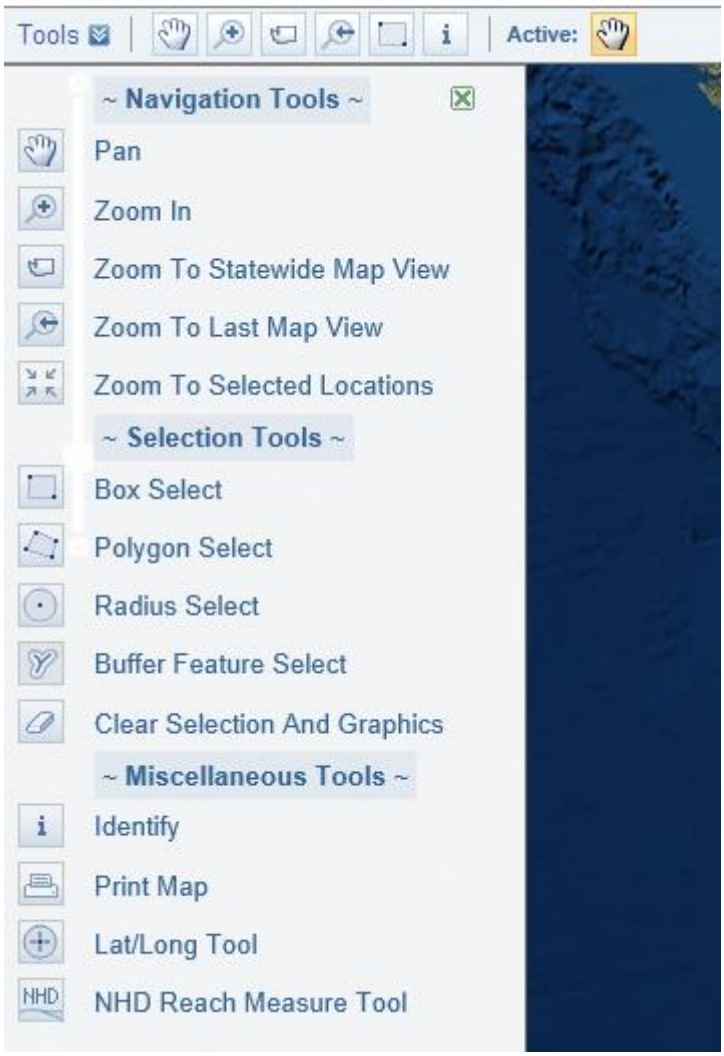
Radius Select - Make selection by drawing a radius around an area. To use:

- Click the Radius Select tool. Next, select a radius distance buffer distance drop-down list. Click a point on the map to center the search from.
- Results: A selection will be made by a radius distance from a center point.

Buffer Feature Select - Selects by drawing a radius around an area. To use:

- Click the Buffer Feature Select tool. Next, select a radius distance buffer distance drop-down list. Next, Choose your target layer from the target dropdown list. Finally, click a point on the map within the feature to buffer.
- Results: A selection will be made within the area of the buffered feature.

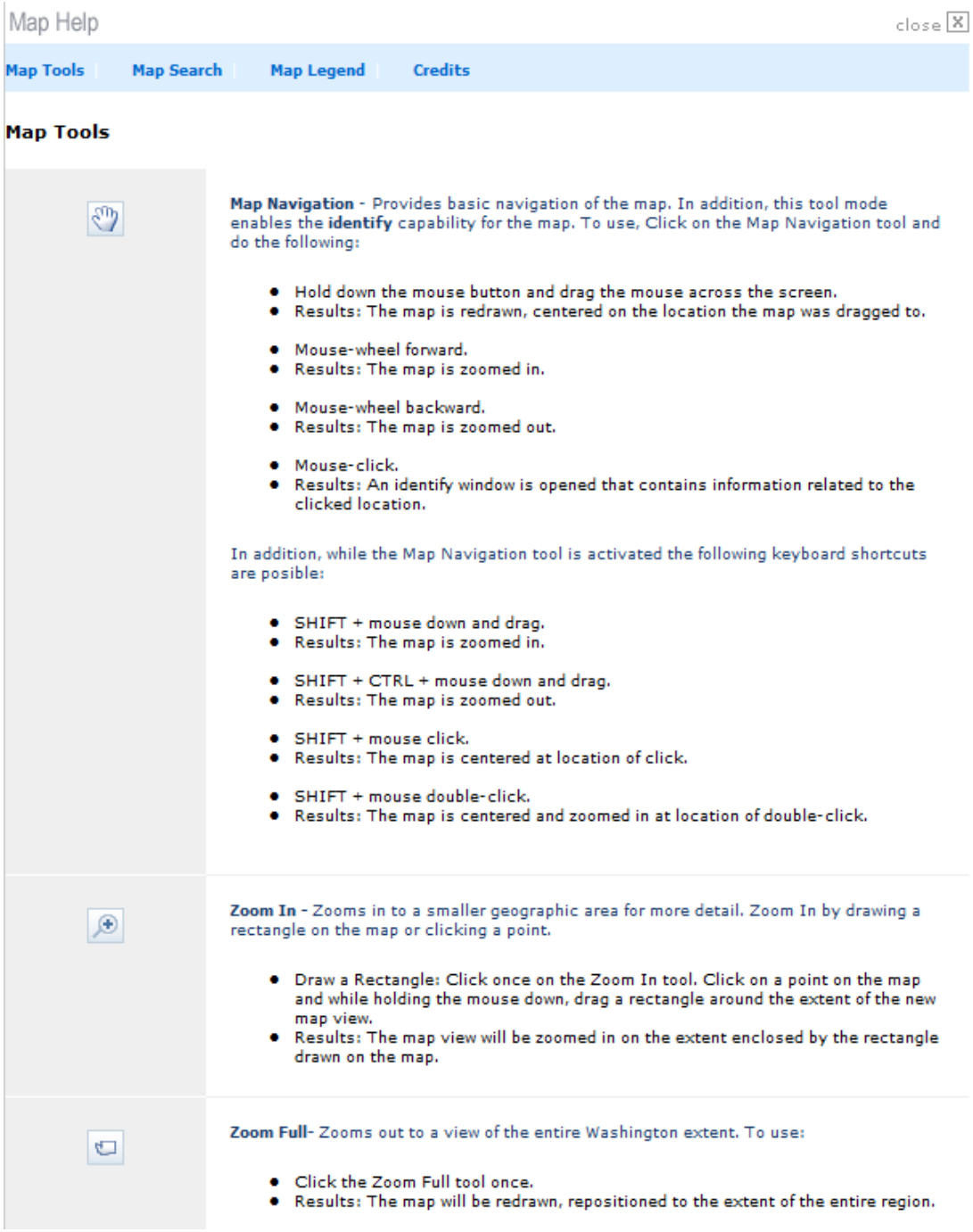
The mapping tool buttons are located on the upper left grey bar as shown below.



Map Viewer Help pages

To get learn how to use these mapping tools, click on the ‘Help’ link located on the top right grey bar of the GIS page.

The screen shots of the Map Help are excerpted below:



Zoom Last - Zooms to the previous map view. To use:

- Click the Zoom Last tool once.
- Results: The map will be redrawn in the previous view.

Zoom to Selection - Zooms map to the extent of the current slection. To use:

- Click the Zoom to Selection.
- Results: The map zooms to the extent of the current selection.

Box Select - Make selection by drawing a box. To use:

- Click the Box Select tool. Next, place the mouse on one corner of the box and hold the mouse button down while moving the cursor to the opposite corner.
- Results: Any facilities touched or enclosed by the polygon will be selected.

Polygon Select - Make Selection by drawing a polygon. To use:

- Click the Polygon Select tool. Next, draw a polygon around your selection by mouse clicking to add a point and double-mouse clicking to finish polygon.
- Results: Any facilities touched or enclosed by the polygon will be selected.

Radius Select - Make selection by drawing a radius around an area. To use:

- Click the Radius Select tool. Next, select a radius distance buffer distance drop-down list. Click a point on the map to center the search from.
- Results: A selection will be made by a radius distance from a center point.

Buffer Feature Select - Selects by drawing a radius around an area. To use:

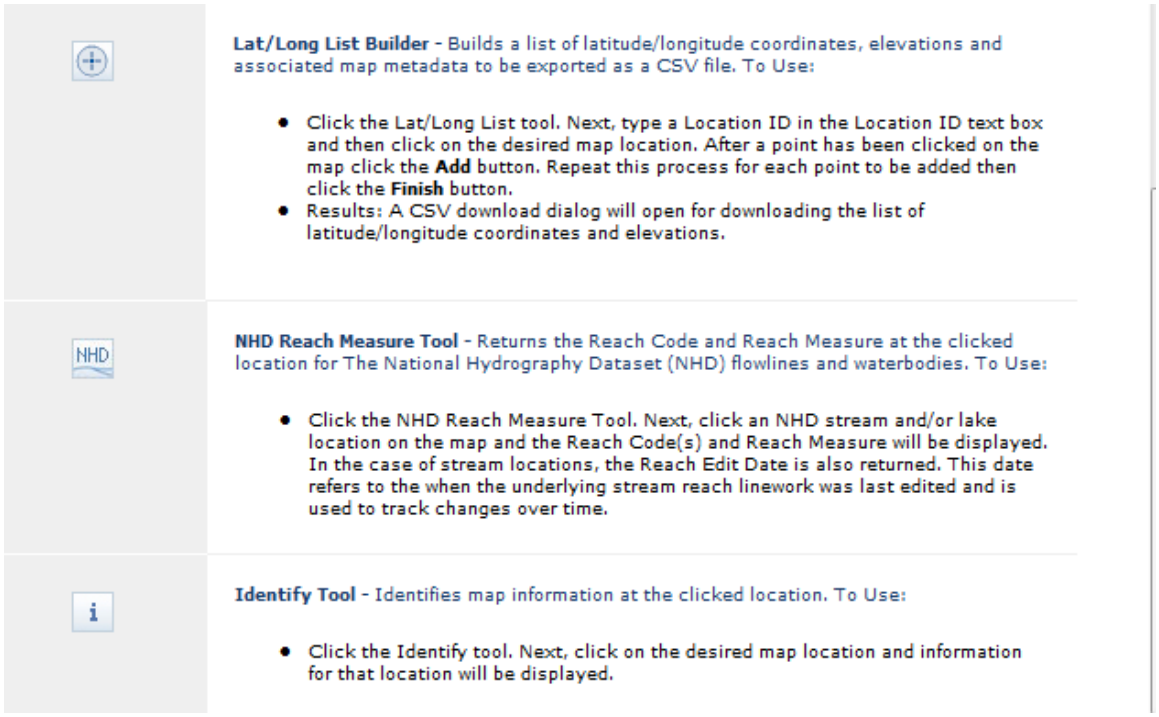
- Click the Buffer Feature Select tool. Next, select a radius distance buffer distance drop-down list. Next, Choose your target layer from the target dropdown list. Finally, click a point on the map within the feature to buffer.
- Results: A selection will be made within the area of the buffered feature.

Clear - Clears selection. To use:

- Click on the Clear button.
- Results: Selection is cleared and the map will be refreshed.

Print Map - Creates a layout page ready for printing. To Use:

- Click the Print Map tool. Next, type a title in the title text box and click the Set Title button. Finally, print the page with your browser's native print functionality.
- Results: A print ready page is created.



Lat/Long List Builder - Builds a list of latitude/longitude coordinates, elevations and associated map metadata to be exported as a CSV file. To Use:

- Click the Lat/Long List tool. Next, type a Location ID in the Location ID text box and then click on the desired map location. After a point has been clicked on the map click the **Add** button. Repeat this process for each point to be added then click the **Finish** button.
- Results: A CSV download dialog will open for downloading the list of latitude/longitude coordinates and elevations.

NHD Reach Measure Tool - Returns the Reach Code and Reach Measure at the clicked location for The National Hydrography Dataset (NHD) flowlines and waterbodies. To Use:

- Click the NHD Reach Measure Tool. Next, click an NHD stream and/or lake location on the map and the Reach Code(s) and Reach Measure will be displayed. In the case of stream locations, the Reach Edit Date is also returned. This date refers to the when the underlying stream reach linework was last edited and is used to track changes over time.

Identify Tool - Identifies map information at the clicked location. To Use:

- Click the Identify tool. Next, click on the desired map location and information for that location will be displayed.

Overview - Tips for Better EIM Mapping

Map Tools

Refresh Map - Generates a new map using the current settings. Use after toggling map layer visibility on or off.

- To Use: Click the Refresh Map button.
- Results: A new map will be drawn.

Select Box - Selects by drawing a box.

- To Use: Click on the Select Box tool. Then place the mouse on one corner of the box and hold the mouse button down while moving the cursor to the opposite corner. To make a selection from the currently selected stations, check the check box found in the tool description pane (found left of the map).

  Results: Locations will be added to current selection. If the select from selected stations check box is checked, a sub-selection of the currently selected stations will be made.

Polygon Select - Selects by drawing a polygon.

- To Use: Click on the Select Polygon tool. Draw a polygon around your selection by left mouse clicking to add a point, double left mouse clicking to finish polygon, and right mouse clicking to cancel polygon. To make a selection from the currently selected stations, check the check box found in the tool description pane (found left of the map).
- Results: Any Locations touched or enclosed by the polygon will be selected. If the select from selected stations check box is checked, a sub-selection of the currently selected stations will be made.

Custom Polygon - Allows user to save and retrieve a polygon for location selection.

- To Use: Click the Custom Polygon button and follow the instructions found left of the map (listed below). To make a selection from the currently selected stations, check the check box found in the tool description pane (found left of the map).
- Results: A polygon saved as a text file to the user's local computer for future use (save function), or a group of selected locations created from saved polygon (load function). If the select from selected stations check box is checked, a sub-selection of the currently selected stations will be made.

Steps (Save Polygon):

1. Draw a polygon if you haven't already created one with the Select Polygon Tool. Draw a polygon by left mouse clicking to add a point, double left mouse clicking to finish polygon, and right mouse clicking to cancel polygon.
2. Click the Save Polygon button and browse to the location on your computer to save the polygon file.
3. Name your polygon file in a meaningful fashion for future retrieval.
4. Click the Save button to finalize polygon save process.

Steps (Load Polygon):

1. Click the Browse button and browse to the location on your computer where you saved your polygon file.

2. Click the Load Polygon button to load polygon and select locations.

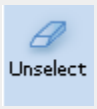
Radius Select - Selects by drawing a radius around an area.

- To Use: Click on the Select Radius tool. To the left of the map, select a radius distance from a center point. Click a point on the map to center the search from. To make a selection from the currently selected stations, check the check box found in the tool description pane (found left of the map).

- Results: Locations will be selected by a radius distance from a center point. If the select from selected stations check box is checked, a sub-selection of the currently selected stations will be made.

Buffer Feature Select - Selects by drawing a buffer around a feature.

- To Use: Click on the Select Buffer tool. Left of the map, select the state of interest. Next, select the desired search distance from the selected map feature. Finally, pick a map layer to make selection from and click on the desired map feature. To make a selection from the currently selected stations, check the check box found in the tool description pane (found left of the map).
- Results: Locations within a defined distance of a selected map feature will be selected. If the select from selected stations check box is checked, a sub-selection of the currently selected stations will be made.



Clear Selection and Graphics – Clears Unselects a selected feature.

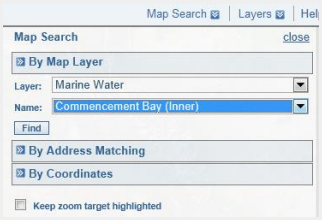
- To Use: Click on the Unselect tool. The selected locations will be cleared.
- Results: The locations will be removed from the selected set and the map will be refreshed.

Print Map - Prepares the map view for printing.

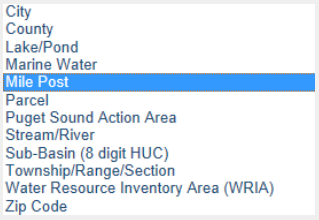
- To Use: Click on the Print Map tool. The Print Map dialog box will open. Enter a map title. Select portrait or landscape. Click on "Create Print Page" to open a new browser window displaying the map formatted for printing.
- Results: You may use the browser's File/Print menu to submit the map to the printer.

Map Search

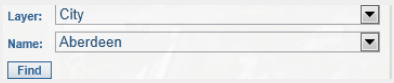
Map Search - Map Search can be done by the Map Layer, Address Matching and Coordinates.



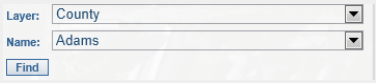
Map Layer – Zoom the map to the specific item of interest from one of the selected map layer list, City, County, Marine Water, Mile Post, Parcel, Puget Sound Action Area, Stream/River, Sub-Basin (8 digit HUC), Township/Range/Selection, WRIA, and Zip Code



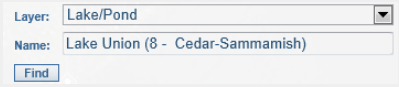
City - Zoom the map to any of the incorporated cities or census-designated places within Washington state. Select a city from the list. The map will zoom to the extent of the selected city. The selected city will be highlighted. Some cities may be made up of several non-contiguous areas.



County - Zoom the map to one of the 39 counties within Washington state by selecting a county from the list. The map will zoom to the extent of the selected county. The selected county will be highlighted.

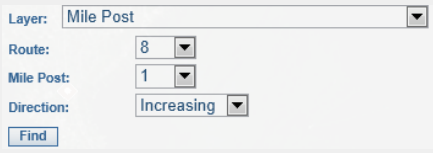


Lake/Pond - Zoom the map to any of the selected Lake/Pond within Washington state. Select a Lake/Pond from the list. The map will zoom to the extent of the selected Lake/Pond. The selected Lake/Pond will be highlighted.



Marine Water - Zoom the map to any of the selected Marine Water in Washington state. Select a bay/inlet/passage/harbor/cove/canal/waterway from the list. The map will zoom to the extent of the selected Marine Water. The selected Marine Water will be highlighted.

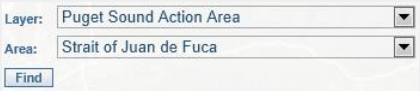
Mile Post - Zoom the map to any of the selected Route/Mile Post in Washington state. Select a Route/Mile Post from the list. The map will zoom to the extent of the selected Route/Mile Post. The selected Route/Mile Post will be highlighted.



Parcel - Zoom the map to any of the selected Parcel in the selected county of Washington state. Select a County from the County list. Type or paste county parcel ID and Click 'Find' button. The map will zoom to the extent of the selected Parcel. The selected Route/Mile Post will be highlighted.

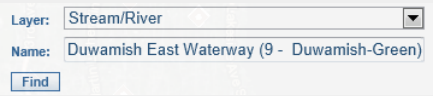
Puget Sound Action Area - Zoom the map to any of the selected Puget Sound Action Area in Washington state. Select a Puget Sound Action Area from the Area list. The map will zoom to the extent of the selected Puget Sound Action Area. The selected Puget Sound Action Area will be highlighted.

Stream/River - Zoom the map to any of the selected Stream/River within Washington state. Select a Stream/River from the Name list. The map will zoom to the extent of the selected Stream/River. The selected Stream/River will be highlighted.

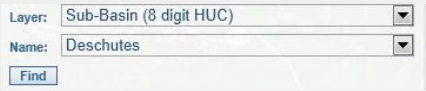


Sub-basin (8 digit HUC) Map - Search by the sub-basin name. The drop down Name lists the sub-basins in the order of their sub-basin name. You will be navigated to the selected sub-basin and it will be highlighted.

What is a sub-basin? The term sub-basin refers to the drainage region based on the 8 digit hydrologic unit code or HUC.



Township/Range/Section - After selecting township, range, and (optionally) section numbers, click the Zoom To button to zoom the map to the selected area. You will be navigated to that township or section and it will be highlighted.



What is township/range/section? The Public Land Survey System defined township, range and section lines in the late 1800's. Townships run north and south and ranges run east and west. Each Township is further divided into a grid of 36 sections. Each section is approximately 1 mile square. The sections are typically numbered 1 through 36. About 5% of the townships use section numbers greater than 36. The sections with numbers above 36 represent Donation Land Claims or other types of early land surveys conducted before the Public Land Survey System was put in place.

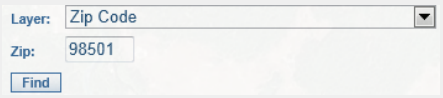
In Washington, township numbers range from 1 North in Clark and Skamania counties to 40 North along the Canadian border. Range numbers go from 16 West in Clallam county to 45 East along the Idaho border.

Watershed (WRIA) Map - Search by the watershed boundary name or its identifying

number. The drop down box lists the watersheds in the order of their identifying number and then states the name of the WRIA. You will be navigated to that watershed and it will be highlighted.

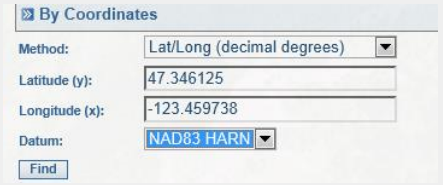
What is a WRIA? The term WRIA means water resource inventory area. A watershed or WRIA is a region that drains into a river or river system.

Zip Code - To zoom to an entire zip code area, type a zip code number into the Zip field. Then click the 'Find' button. The map will zoom to the extent of the searched zip code. The zip code area will be highlighted in yellow.



Address Matching - Zoom the map by entering a street address, City and Zip Code, then clicking the 'Find' button. If the entered address is matched in the street database, the map will zoom to the matched street address. The found address will be highlighted on the map.

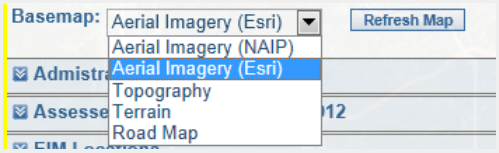
Coordinates - To zoom to a specific NAD83 HARN decimal degree longitude/latitude coordinate, type a longitude value into the Longitude field and a latitude value into the Latitude field (valid longitude values range from -116 to -126 and valid latitude values range from 44 to 50). Select NAD83 HARN from the Datum dropdown list. Finally, click the 'Find' button. The map will zoom to the extent surrounding the longitude/latitude pair.



Map Layers

- Under the **Map Layers** tab, a list of available map layers is displayed. The layers are categorized and stored inside folders by topic.
- The folders can be opened and closed. The visibility of the layers can be toggled on and off.

- A **background image** can also be selected under Basemap. Only one background image can be displayed from five basemaps at a time. The Aerial Imagery (Esri) is on by default. The following five basemaps are
- The **Water Bodies** layer (found in the Hydrographic Features folder of the **Map Layers** tab) may be turned off to view the full extent of the background imagery.



EXERCISE 5: CREATE A LOCATION GROUP FROM THE MAP

(1) From MyEIM Home page, Custom Groups section, click on the 'Location' link. You will be redirected to the custom groups list interface for locations.

(2) Click the 'New Location Group using GIS interface' button. You will be redirected to the GIS (EIM Map Viewer) page.

(3) Under Map Layer located on the upper right hand side of the grey navigation bar, select City Layer, Olympia under Name, and click 'Find'.

(4) Select Terrain in Basemap from the Map 'Layers'.

(5) Zoom to the Capital Lake area of interest using the 'Zoom In' tool. The current tool select is 'Zoom'. Drag a rectangle into the Capital Lake area of interest.

(6)You have zoomed into your area of interest. Now, select the 'Polygon Select' tool and draw a polygon around the Capital Lake on the map. The selected locations will turn blue with the locations labeled with their names by checking 'Show Labels' for the Selected EIM Locations under EIM Locations from the 'Layers'.

(7) Click the 'View Data' button. By clicking the 'View Data' button, you will be redirected to the custom groups interface for locations. The custom groups interface will display a table of records of your selected locations. This is exactly the same interface used to create a location group using tabular criteria.

(8) You can optionally delete individual locations from the table of records if desired.

(9) Click the 'Save Custom Group' button and provide a 'Custom Group Name' and optionally a 'Description' then click the 'Save My Location Group'.

(10)Your user defined location group, Capital Lake, is now available to be used as a search criteria item. Refer to the Home Page chapter on using your location group within a search. To return to the MyEIM Home page, click on the "My EIM Home" link. Select 'Chemistry Study Check' under Search templates. Clicking on 'Save As' will bring you to the Chemistry Search page.

(11) Edit Search Criteria. Select 'Groups' under Category, User Defined – Location Group under Field Name, Equal under Operator, and select Capital Lake under Value dropdown list.

(12) Clicking on "Show Data' will bring you to the Results page for the EIM chemistry data in the Capital Lake.

This completes exercise 5.

LAB 5: CREATE A LOCATION GROUP FROM THE MAP (ALTERNATE)

In the previous chapter, you have created a location group from the Results interface by clicking the ‘Create Group’ link and select ‘Location Group’ upon saving a group.

Perform a search then click ‘Go to Map’.

Modify the data by adding/removing locations from the map then click the ‘View Data’ button.

You will return to the results interface. Click on the ‘Create Group’ link and select ‘Location Group’.

This is another way to create location groups from the map (using the map to modify data).

Also in this lab, read the ‘Map Help’ and use other select tools the GIS interface has to offer such as ‘Box Select’, ‘Polygon Select’, ‘Radius Select’ and ‘Buffer Select’ under Selection Tools and ‘Map Layer’, ‘Address’, ‘Coordinates’ under Map Search. .

EXERCISE 6: BUFFER AN ADDRESS BY 2 MILES

(1) From the portal interface under the Custom Groups, click on the Location link. You will be taken to the custom groups list page for locations. Click the New Location Group using GIS Interface button. You will see the Map Viewer with a map of Washington State.

(2) Click the Map Search tab in the top left of your screen. Now enter your Street Address = "300 Desmond Dr", Zip code = "98503" and then click the 'Find' button and your address of interest will be highlighted on the map. Note, you must include the real and complete house number, street, direction, and zip code. Do not add city or state information to the street address.

(3) Click the Radius Select tool located under the Tools dropdown list. Set the Radius distance to 2 miles and click the at the highlighted address on the map.

(4) Your map will draw the red buffer circle and selected the sampling locations (blue for selected locations and brown for non-selected locations) within two miles of your address.

(5) Now click on the 'View Data' button and that should take you back to Location Group page with the selected locations displayed.

(6) To save this group, click on the 'Save Custom Group' button, enter values for the Name = "300 Desmond Drive" and Description = "2 Mile Buffer" and click 'Save My Location Group' (GIS) to finish.

(7) Click on the "My EIM Home" link to go back to the 'portal' interface then click 'Chemistry' search from the Custom Search section. In the Search interface, under the Add Search Criteria, select the value of Groups from the "Category" column. Then, select the value of User Defined – Station Group from the "Field Name". Leave the value of Equals in the "Operator" column. Choose Value = "300 Desmond Dr". Now click on "Update" button to the right.

(8) Click the 'Add Criteria' button. Add Search Criteria, select the value of Result from the "Category" column. Now select the value of Result Parameter Name from the "Field Name". Leave the value of Equals in the "Operator" column. Enter Value = "Arsenic". Then click on "Update" button to the right.

(9) Click the Show Data button. Your records will display.

This completes exercise 6.

EXERCISE 7: FIND PCB LOCATIONS IN COMMENCEMENT BAY

(1) From MyEIM Home page under the Custom Groups, click on the 'Location' link. Clicking the 'New Location Group using GIS interface' button will bring you to the EIM Map Viewer page.

(2) Click the Layers tab in the upper left hand corner. Under the Administrative Boundaries, check the City tab. Under the Map Layers tab, a list of available map layers is displayed. The layers are categorized and stored inside folders by topic.

(3) Click the Map Search tab in the upper right hand corner and from the City drop down list select Tacoma. Choose the select buffer tool, enter 0 miles, choose Cities, and click in Tacoma on the map. Your Selected Locations will appear on the map.

(4) Click on the View Data button. Click on the Save Search button, set the name = "Tacoma", description = "Stations in Tacoma" then click the Save My Location Group (GIS) button.

(5) From the 'portal' page click MyEIM Home. Click on the Edit Location Group from the Map button which will take you to the Map Viewer. Click on the Select Polygon tool and draw a polygon around Commencement Bay.

(6) Then click on the View Data button and that should take you back to Location Group page with the selected locations displayed. Save this group, click on 'Save Custom Group' Search button key in the Custom Group N*ame* = "Tacoma – Commencement Bay" D*escription* = "Stations in Tacoma and Commencement Bay" and click 'Save My Location Group' to finish.

(7) From the 'portal' page click Custom Search. In the Search definition page, under the Add Search Criteria, select the value of Groups from the "Category" column. Then, select the value of User Defined – Station Group from the "Field Name"**.** Leave the value of Equals in the "Operator" column**.** Choose Value = "Tacoma – Commencement Bay". Then click on the "Update" button.

(8) Click the Add Criteria button. Add Search Criteria, select the value of Results from the "Category" column. Then, select the value of Result Parameter Name from the "Field Name"**.** Leave the value of Equals in the "Operator" column**.** Enter Value = "PCB". Then click on the "Update" button to the right.

(9) Click the Show Data button. Your records will display.

This completes exercise 7.

EXERCISE 8: FIND AMMONIA LOCATIONS ALONG THE SPOKANE RIVER

(1) From the portal interface under the Custom Groups, click on the Location link. Click the 'New Location Group using GIS Interface' button. The Map Viewer will appear.

(2) Click the Map Search tab in the upper left hand corner. Enter the Longitude = "-117.409198" and enter the Latitude = "47.663373". Click the 'Find' button. Click the 'Buffer Feature Select' button, Choose 0.5 mile buffer from the Target Watercourse. Click on the selected coordinates on the map viewer will draw a map with your red lined buffer (shaded area) around the selected locations.

(3) Click on View Data. Click on the 'Save Custom Group' button and set the name = "Spokane River", description = "Locations within 0.5 miles of the Spokane River" then click the 'Save My Location Group' button.

(4) From the Home page, click Custom Search. In the Search Interface, under the Add Search Criteria, select the value of Groups from the "Category" column. Then, select the value of User Defined – Location Group from the "Field Name". Leave the value of Equals in the "Operator" column. Choose Value = "Spokane River". Then click on "Update" button. Enter the following additional criteria items.

Category	Field Name	Operator	Value
Result	Result Parameter Name	Equals	Ammonia
Sample	Sample Matrix	Equals	Water
Result	Result Value	Greater Than	0.1 mg/L

(5) Click the Show Data button. Your records will display.

This completes exercise 8.

Chapter 5: Sediment Chemistry Analysis

The MyEIM Analysis application provides the tools to perform criteria comparison and statistical analysis of sediment chemistry results queried through the quick start search in Search Templates or your saved search in My Custom Searches or chemistry search in Custom Search.

OVERVIEW OF SEDIMENT CHEMISTRY ANALYSIS

The MyEIM Analysis application provides tools to compare the searched results of interest to selected cleanup standards (also known as cleanup criteria). The SMS criteria are available under 'Cleanup Criteria' tab in MyEIM. Users are not restricted to compare searched results to predefined cleanup standards. MyEIM Analysis provides an interface for you to define your own set of standards and derived variables using user defined cleanup criteria and user defined derived variables.

This chapter consists of three sections, Sediment Chemistry Data Search, Standard Analysis and Customizing My Analysis. Sediment Chemistry Data Search will show you the steps necessary to perform in preparation for data analysis. Standard Analysis will cover the use of predefined cleanup criteria as the basis of analysis. Customizing My Analysis will discuss various user definable aspects of the application. Several exercises will help demonstrate the use of the various features. At the end of this chapter, sample scenarios are presented to show real-world scenarios of how to utilize the system.

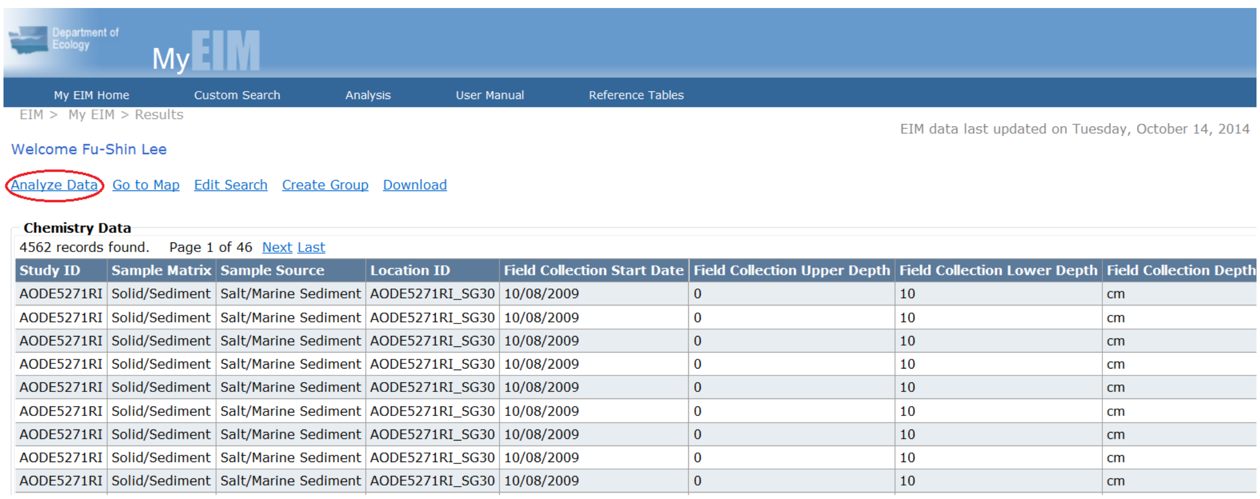
Note: Before we begin, this chapter assumes that you have already acquired a data result set using the Search application. If you do not have a result set to work with, refer to the Home and Search chapters.

SEDIMENT CHEMISTRY DATA SEARCH

To begin the analysis process, you will first have to get a result set from the quick start search template (Chemistry sediment data check) in Search Templates or your saved search in My Custom Search or chemistry search in Custom Search.

Note: If you need a quick sediment chemistry result set to get started, select ‘Chemistry sediment data check’ in Search Templates of the ‘Home’ page. Clicking on ‘Save As’ will bring you to the ‘Chemistry Search’ page. Clicking on ‘Show Data’ will bring you to the Results page for the searched Chemistry Data.

On the searched Results page for Chemistry Data, click the ‘Analyze Data’ link in the upper left corner of the content page. This link will take you to the “Choose Comparison Criteria” page of the Analysis application.



Study ID	Sample Matrix	Sample Source	Location ID	Field Collection Start Date	Field Collection Upper Depth	Field Collection Lower Depth	Field Collection Depth
AODE5271RI	Solid/Sediment	Salt/Marine Sediment	AODE5271RI_SG30	10/08/2009	0	10	cm
AODE5271RI	Solid/Sediment	Salt/Marine Sediment	AODE5271RI_SG30	10/08/2009	0	10	cm
AODE5271RI	Solid/Sediment	Salt/Marine Sediment	AODE5271RI_SG30	10/08/2009	0	10	cm
AODE5271RI	Solid/Sediment	Salt/Marine Sediment	AODE5271RI_SG30	10/08/2009	0	10	cm
AODE5271RI	Solid/Sediment	Salt/Marine Sediment	AODE5271RI_SG30	10/08/2009	0	10	cm
AODE5271RI	Solid/Sediment	Salt/Marine Sediment	AODE5271RI_SG30	10/08/2009	0	10	cm
AODE5271RI	Solid/Sediment	Salt/Marine Sediment	AODE5271RI_SG30	10/08/2009	0	10	cm
AODE5271RI	Solid/Sediment	Salt/Marine Sediment	AODE5271RI_SG30	10/08/2009	0	10	cm
AODE5271RI	Solid/Sediment	Salt/Marine Sediment	AODE5271RI_SG30	10/08/2009	0	10	cm

Figure 1 - MyEIM Results Page

Custom Search hands off the results at the back end to Analysis when you come into the Analysis application.

STANDARD ANALYSIS

Two following pages for chemistry data analysis will be shown in the order of analysis process:

1. Choose Comparison Criteria
2. Analysis Results

CHOOSE COMPARISON CRITERIA PAGE

The first step in the Analysis process is to collect settings for the analysis on the data received from the Chemistry Search application. The *'Choose Comparison Criteria'* page is the first step in analyzing your data. It is important to note the different elements of this page which consist of the following components:

At the top of the page (Figure 2) is the Welcome banner displaying user's name and MyEIM navigation menu. Below this banner is the data Analysis Type (e.g., Sediment Chemistry, MTCA, Tissue Chemistry) and Selected Standards list box which displays the standards you have selected to compare your searched chemistry data against. To the right of the Analysis and Selected Standards is the 'Selected Preferences' summary. A prominent 'Compare' button is just below the Selected Preferences summary detail container. The Show All Standards checkbox sits below the 'Clear Selected Standards' link. The Criteria and Variables grid is the main grid on the page, organized by a set of page tabs, Cleanup Criteria, User Defined Cleanup Criteria, Derived Variables and User Defined Derived Variables, which allows the users to select established and/or user defined cleanup criteria, and to create user defined cleanup criteria and derived variables. Clicking on the blue arrow next to the selected standard or variable will show you the constituents of the selected criteria and variable at the bottom of the page in Figure 3.

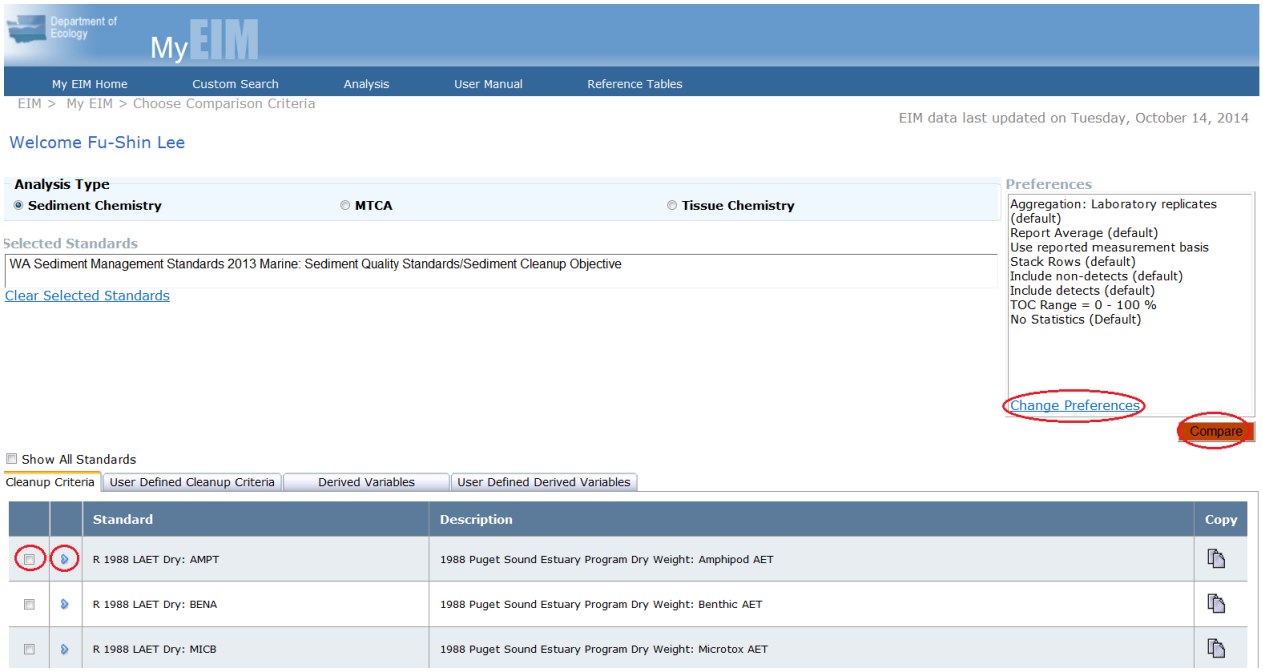


Figure 2 - MyEIM Analysis - Choose Comparison Criteria page

The options and features in the 'Choose Comparison Criteria' page are detailed below.

Analysis Type

MyEIM supports analysis of sediment data, MTCA data (soil and water), and tissue data. These three types of analyses differ in the data reduction logic and statistical options. MyEIM will identify the most matching analysis type based on the specific sample source of data you search. Sediment Chemistry was selected in this screen shot, since Salt/Marine Sediment was selected for Sample Source in MyEIM Chemistry Search page. Users need to decide what type of analysis is appropriate for the data obtained from custom query. MyEIM is currently designed to analyze one sample source of searched data each time.

Note: Users can apply MTCA analysis type to sediment data or use any other mismatching combinations. However, user needs to be aware that the underlying data reduction logic and output results depend on the selected analysis type that goes into MyEIM analysis processors.

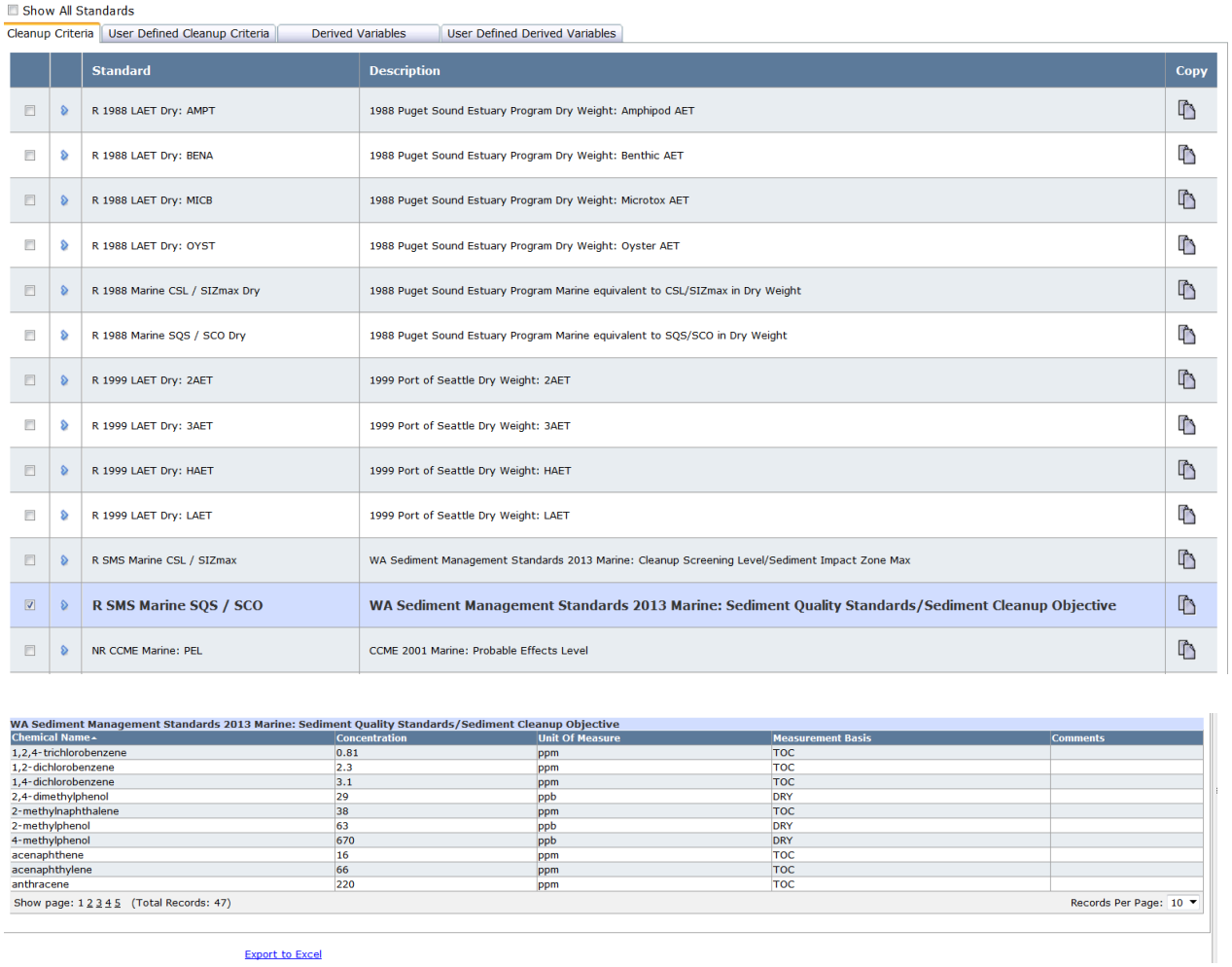


Figure 3 - MyEIM Analysis – Selected SMS Marine SQS / SCO on Choose Comparison Criteria page

CLEANUP CRITERIA

Cleanup Criteria is one of four options under the Cleanup Criteria and Derived Variables grid. MyEIM Cleanup criteria have all the regulatory SMS sediment criteria and non-regulatory criteria for marine sediment and freshwater sediment. MyEIM will display the applicable sediment cleanup criteria per selected specific sample source of searched chemistry data. For example, when marine/salt sediment is selected as the sample source of the searched chemistry data, cleanup criteria will automatically display the SMS marine criteria and non-regulatory criteria. The criteria housed under Cleanup Criteria will be updated, when the regulatory or non-regulatory criteria are updated.

Selected Standards

This box will display the list of standards (also called ‘comparison criteria’) that have been selected to use for chemistry data analysis. Criteria are added or removed from this box by checking or un-checking the rows in the Cleanup Criteria and User Defined Cleanup Criteria grids.

Selected Preferences

The selected Preferences summary box displays the analysis and statistical options that will be used during the execution of the analysis. You have access to the ‘Analysis Criteria’ and ‘Statistical Parameters’ settings by clicking the ‘Change Preferences’ link at the bottom left corner of the Preferences box. After you review the review and select your ‘Analysis Criteria’ and ‘Statistical Parameters’ settings, in order to return to the Choose Comparison Criteria page, click ‘OK’ to accept your changes or ‘Cancel’ button to accept default existing settings.

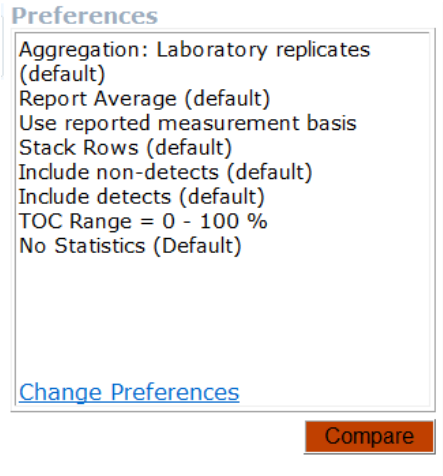


Figure 3a - Default Settings for Sediment Chemistry Data Analysis in Preferences Box

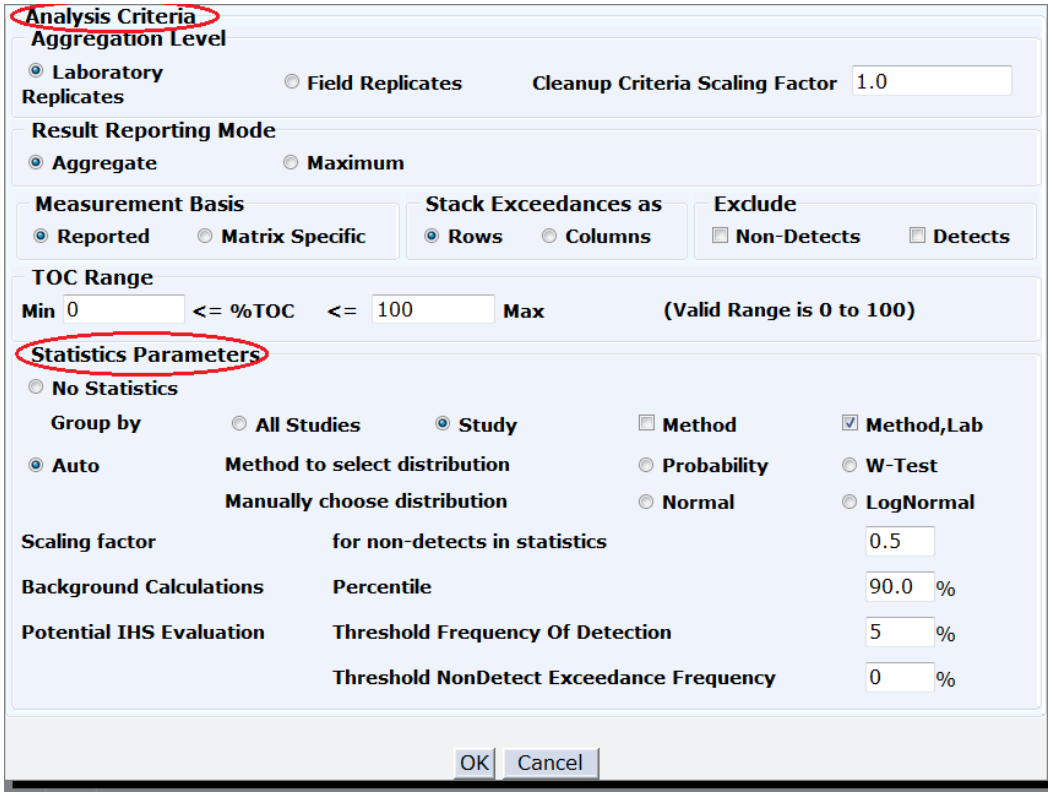


Figure 3b – Select study and Method, Lab in Preferences Dialog for Sediment Chemistry

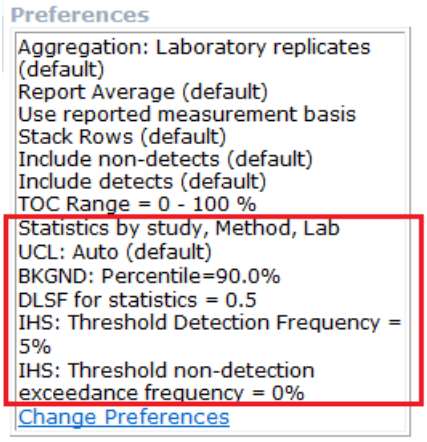


Figure 3c - Selected Statistical Settings in Preferences Box

The Preferences pop up window (Figure 3b) has two major groups of options, Analysis Criteria and Statistical Parameters.

The option groups in ‘Analysis Criteria’ have settings for how the data will be aggregated for criteria comparison and derived variable calculations, how the data will be compared to the adjusted cleanup criteria using Cleanup Criteria Scaling Factor, as well as output results display options. The options for Analysis Criteria will be detailed under ANALYSIS CRITERIA.

The ‘Statistics Parameters’ group has settings used exclusively for statistical analysis. The ‘Statistics Parameters’ group has settings used exclusively for sediment data statistical analysis (Method and lab). However statistical analysis and display depend on all analysis and statistical settings.

ANALYSIS CRITERIA

Aggregation Level

Laboratory Replicate data aggregation will aggregate all laboratory replicate results and give one value for the sample reporting laboratory replicate results in EIM. Field Replicate data aggregation will aggregate all field replicate results and give one value for the sample reporting field replicate results in EIM. Laboratory Replicates level is chosen by default for Sediment Chemistry Analysis Type. Field Replicates level is chosen by default for MTCA Analysis Type. Please refer to Appendix E for details on how these rules are implemented.

Result Reporting Mode

This sets the rule for data reduction. It provides two options: Aggregate rule and Maximum rule. Please refer to Appendix E for details on how these rules are implemented.

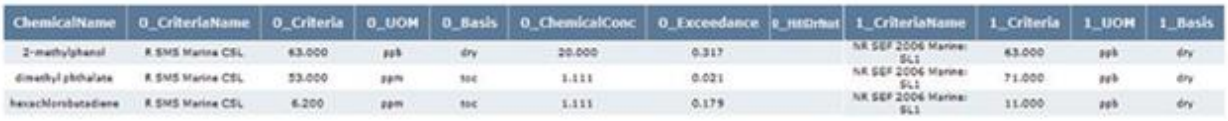
Measurement Basis

By default, reported result measurement basis is used for all calculations. MyEIM will automatically assign dry for soil/sediment sample and wet for water samples. In cases where measurement basis is wrongly reported, MyEIM allows users to override the reported measurement basis with a matrix specific measurement basis (assign ‘dry’ for all sediment data except where reported basis is ‘toc’). In order to assign an override value automatically where appropriate, you will need to select ‘Matrix Specific’ option.

Stack Exceedances As

"Stacking Exceedances" refers to the output of the analysis results. Let's take as an example a comparison with two criteria.

If Stack Exceedances is set to "Columns," then for each row in the data results, there will be one row in the analyzed results. Each of these rows will have full sets of analysis columns, one for each chosen criteria. This option is currently not working, and will be addressed when the end users see the strong needs of using it.



ChemicalName	0_CriteriaName	0_Criteria	0_UOM	0_Basis	0_ChemicalConc	0_Exceedance	0_HitOrNot	1_CriteriaName	1_Criteria	1_UOM	1_Basis
2-methylphenol	R SMS Marine CSL	63.000	ppb	dry	20.000	0.317		NR SEF 2006 Marine: SL1	63.000	ppb	dry
dimethyl phthalate	R SMS Marine CSL	53.000	ppm	toc	1.111	0.021		NR SEF 2006 Marine: SL1	71.000	ppb	dry
hexachlorobutadiene	R SMS Marine CSL	6.200	ppm	toc	1.111	0.179		NR SEF 2006 Marine: SL1	11.000	ppb	dry

Figure 4a – Analyzed results stacked in columns. Notice the 0_ and 1_ in front of the column names.

The "Rows" is selected by default, the grid will have multiple analyzed rows for each data result; one for each chosen criteria group.

ChemicalName	CriteriaName	ChemicalConc	CriteriaConc	CriteriaUOM	CriteriaBasis	Exceedance	HitOrNot
arsenic	R SMS Freshwater CSL	20	120	mg/kg	dry	0.1667	
arsenic	R SMS Freshwater SCO	20	14	mg/kg	dry	1.429	Hit

ChemicalName	CriteriaName	Criteria	UOM	Basis	ChemicalConc	Exceedance	HitOrNot
2-methylphenol	R SMS Marine CSL	63.000	ppb	dry	20.000	0.317	
2-methylphenol	NR SEF 2006 Marine: SL1	63.000	ppb	dry	20.000	0.317	
dimethyl phthalate	R SMS Marine CSL	53.000	ppm	toc	1.111	0.021	
dimethyl phthalate	NR SEF 2006 Marine: SL1	71.000	ppb	dry	20.000	0.282	
hexachlorobutadiene	R SMS Marine CSL	6.200	ppm	toc	1.111	0.179	
hexachlorobutadiene	NR SEF 2006 Marine: SL1	11.000	ppb	dry	20.000	1.818	Hit

Figure 4b – Analyzed results stacked in rows. Notice Chemical Name is duplicated for each criteria group.

Exclude

Check the box next to either Detects or Non-Detects to exclude them from the results output (Selecting both Non-Detects and Detects will forcefully exclude ALL results output).

TOC Range

Set the Total Organic Carbon (TOC) concentration minimum value and maximum value. Results that have a reported TOC value outside of the range entered here will be excluded.

Statistics Parameters

MyEIM allows users to compute statistics on data reduced concentrations for every chemical reported in each study through 'Study' or across all studies through 'All Studies' or in combination with Method or Method and Lab. Please refer to the chapter on MTCA Statistics for details. Select All Studies to identify potential indicator hazardous substances, to calculate background and 95% UCL of the mean. Select Study and Method and Lab to analyze and verify the data versus the SAP / QAPP and the data report package

Compare Button

Clicking this button will begin the analysis processing and bring you to the Analysis Results page, when the analysis is completed. All of the settings you have chosen will be sent to MyEIM processors for analysis.

Clear Selected Standards

Clicking this link will unselect both standard and user defined cleanup criteria listed in selected standards list.

Show All Standards Checkbox

By default, this box remains unchecked. In this case, only the criteria that have the same sample matrix and sample source as your search results will appear under the "Standard Cleanup Criteria" tab.

If the 'Show All Standards' box is checked, all standard criteria will be displayed, including those that can't be matched to your search results based on sample matrix and sample source.

Note: The analysis processor will compare search results to any standards even if they are incompatible in terms of sample matrix and sample source. This feature is made available for cross media analysis, however, caution is advised. In any case, the comparison will be made only if measurement basis and unit of measurement are compatible with those of the chosen criteria.

Criteria and Variables Grid

The Criteria and Variables grids display Standard Cleanup Criteria, User Defined Cleanup Criteria, Derived Variables and User Defined Derived Variables, and constituents in each of these four types of criteria and variables items. These four grids are discussed in more detail below.

Constituents List

The Constituents List displays detailed information for the selected criteria or derived variable. This includes chemical name, measurement basis, cleanup concentration, and unit of measure. This list can be exported to excel for further analysis.

Cleanup Criteria tab

The simplest analysis that can be performed is to select an existing standard under the Cleanup Criteria tab, and then click the Compare button. The list of constituents associated with each standard can be viewed by clicking the blue arrow located next to the check-box (figure 3). This list can also be exported to Excel.

User Defined Cleanup Criteria tab

Users can customize cleanup criteria in the user defined cleanup criteria and use those criteria for comparison. This will be discussed in more detail later in this chapter.

Derived Variables tab

This tab lists available standard derived variables. There are two types of standard derived variables, Simple Derived Variables and Weighted Derived Variables. Simple derived variables had all constituents equally weighted. In weighted derived variables, constituent weights are fractions. Simple derived variables include Total Benzofluoranthenes (BFA), Polychlorinated Biphenyls (PCBs), Low Molecular Weight Polycyclic Aromatic Hydrocarbons (LPAH), High Molecular Weight Polycyclic Aromatic Hydrocarbons (HPAH), PCB Aroclor Sum, PCB Congener Sum, Total PAHs, Total DDDs, Total DDEs, Total DDTs and Particle/Grain Size, Fines (Silt/Clay). Weighted derived variables include Carcinogenic Polycyclic Aromatic Hydrocarbons as TEQs (cPAH-TEQ), Dioxin/Furan-TEQ, Dioxin-like PCB TEQ and Total 2,3,7,8-TCDD TEQ. Percent Fines and weighted derived variables need to be defined in the user defined cleanup criteria in order to be calculated, compared to the criteria and displayed in the results output.

User Defined Derived Variables tab

Users can customize derived variables under User Defined Derived Variables tab and use them in the User Defined Cleanup Criteria. This feature will be discussed later in this chapter.

EXERCISE 1: COMPARING TO PREDEFINED CLEANUP CRITERIA

(1) In the Chemistry Search page, build one of the following four queries. For example in the first query, set Category to 'Study', Field Name to 'User Study ID', set Value to 'PSDDA_00', click the 'Update' button. Set Category to 'Sample', Field Name to 'Sample Source, set Value to 'Salt/Marine Sediment', click the 'Update' button.

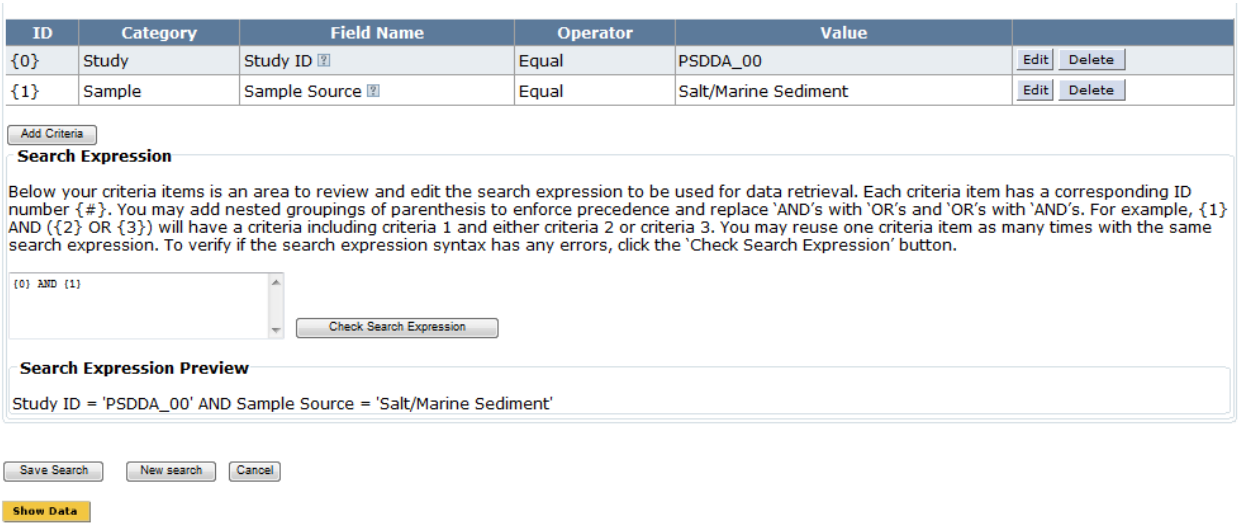


Figure 5 – Building a simple sediment query

Click 'Show Data'.

(2) This will take you to preview of the 'Results' page for Chemistry Data.

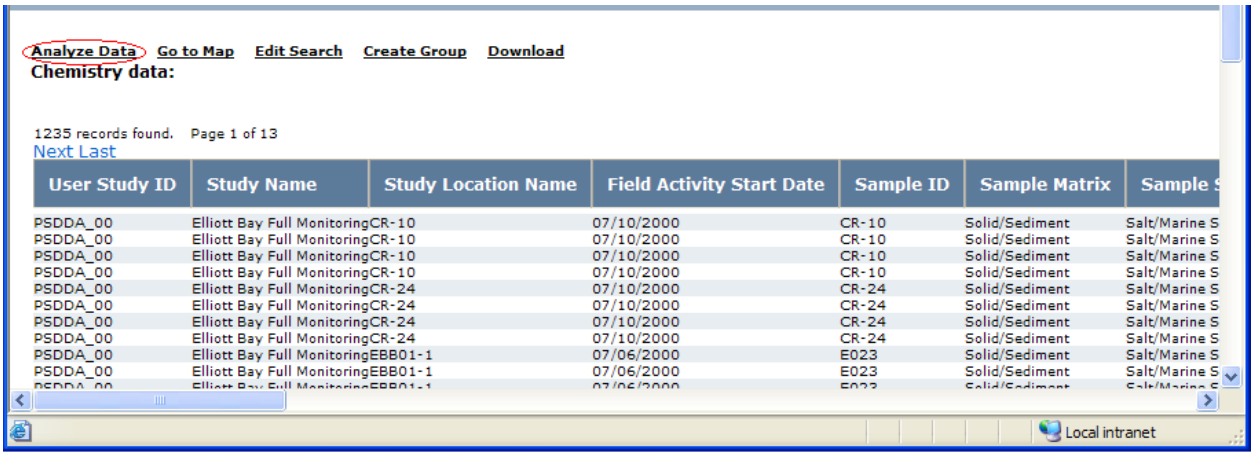


Figure 6 - Query results page

Click on ‘Analyze data’.

(3) Begin by clicking the checkbox for R SMS Marine SQS/SCO from the Standard Cleanup Criteria tab.

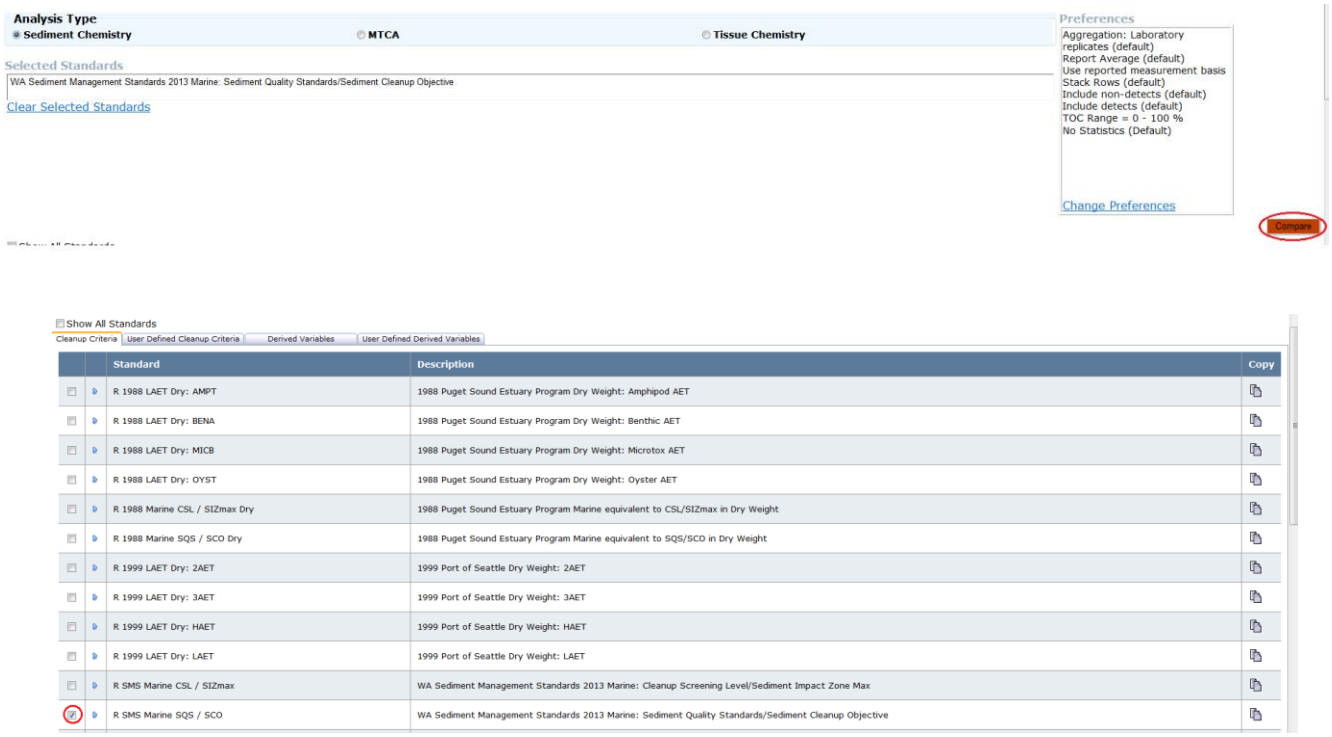


Figure 7 – SMS Marine SQS Selected

Note: Once you select an item from the list, it will be added into the Selected Standards.

(4) Click the Compare button. You will be transferred from this page to the Processor page while the analysis is being performed.

(5) This page will display the process status, along with the total number of rows received from the database and from analysis.

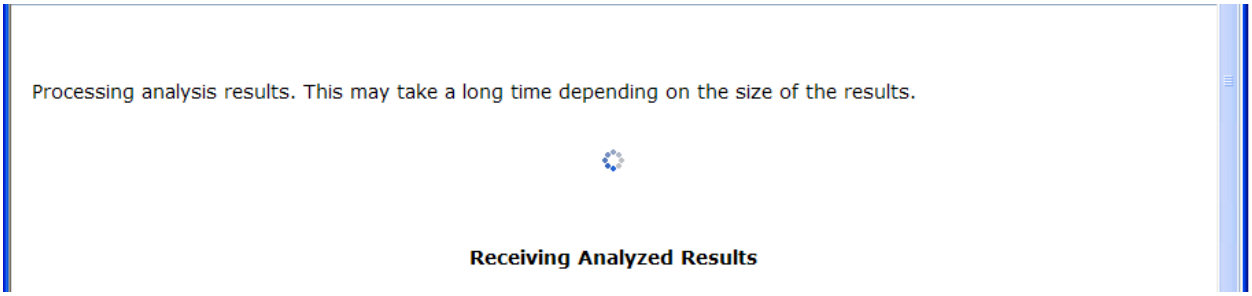


Figure 8 – Analysis processing update real time message

As the database is streaming the data to the chemistry analysis processors, processors will perform the analysis and start to display queried and processed results counts. When analysis processing is complete, the Analysis Results page is displayed with results of your analysis.

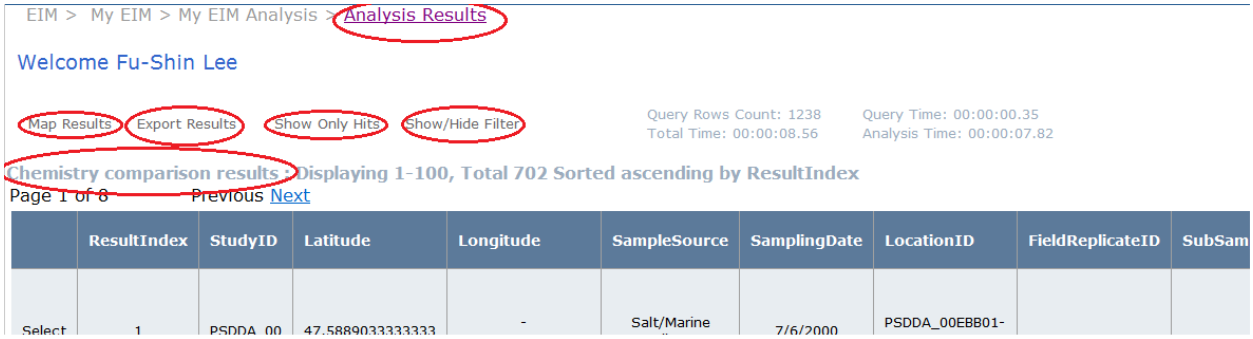
Figure 9 - Display Results page

You have taken a result set and compared it with the selected cleanup criteria. The results of the analysis are laid out in two grids. The top grid is the Chemistry Comparison Results grid. Below this grid is a grid with derived variables calculation details.

Note: Derived variable calculation will be performed only when a standard is selected that had derived variables listed for comparison. Field replicate aggregated results will not display derived variable calculation results.

ANALYSIS RESULTS PAGE

Results are displayed on the screen through the Analysis Results page. From here you can map the analyzed results through 'Map Results', filter the results down to a smaller subset of the full analyzed dataset through 'Show/Hide Filter' or 'Show Only Hits', or export the results to a spreadsheet file through 'Export Results' and 'Export Statistics' when analyzed and available. These key functions, 'Map Results', 'Show/Hide Filter', 'Show Only Hits', 'Export Results' and 'Export Statistics', will be detailed in the exercises.



The Analysis Results page contains two or three grids, depending on whether the statistical parameters are selected.

1. Chemistry comparison results
2. Derived variable results
3. Statistics variable results

Each grid on this page provides paging through the data 100 rows at a time. This is done by clicking the Previous and Next buttons on the top of the grid. The total number of rows is displayed in the grid title.

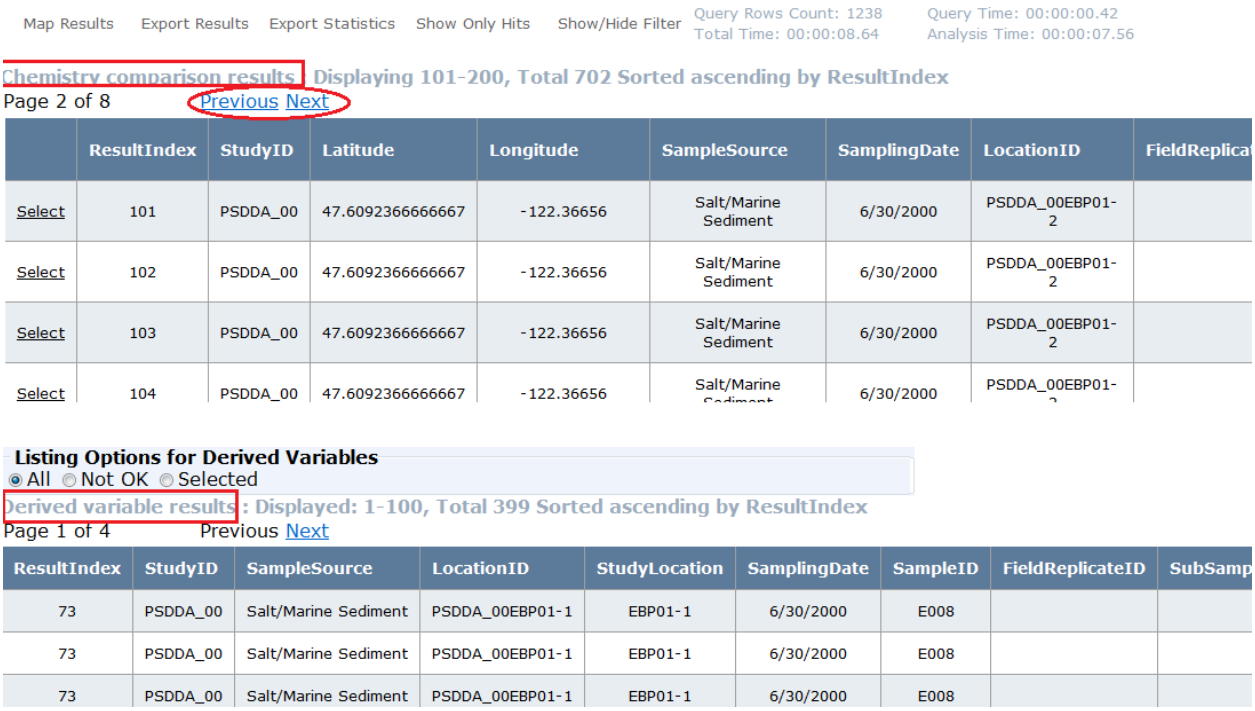


Figure 10a - Display Results page contains two grids: criteria comparison and derived variables.

Chemistry Comparison Results Grid

The upper grid contains the Chemistry Comparison Results. Chemical concentrations at the chosen replicate level are aggregated, then normalized with respect to the unit of measure (Result Value Units for searched EIM chemistry results) and measurement basis (Result Basis for searched EIM chemistry results) of the cleanup criteria before calculating the ratio (chemical concentration divided by criteria concentration) of concentration values to find Exceedance.

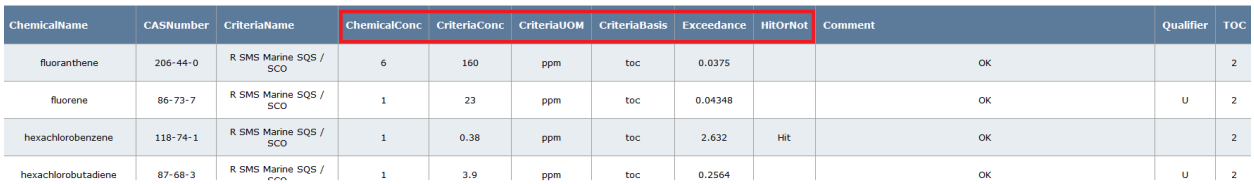


Figure 10a – Chemistry Comparison Results Grid

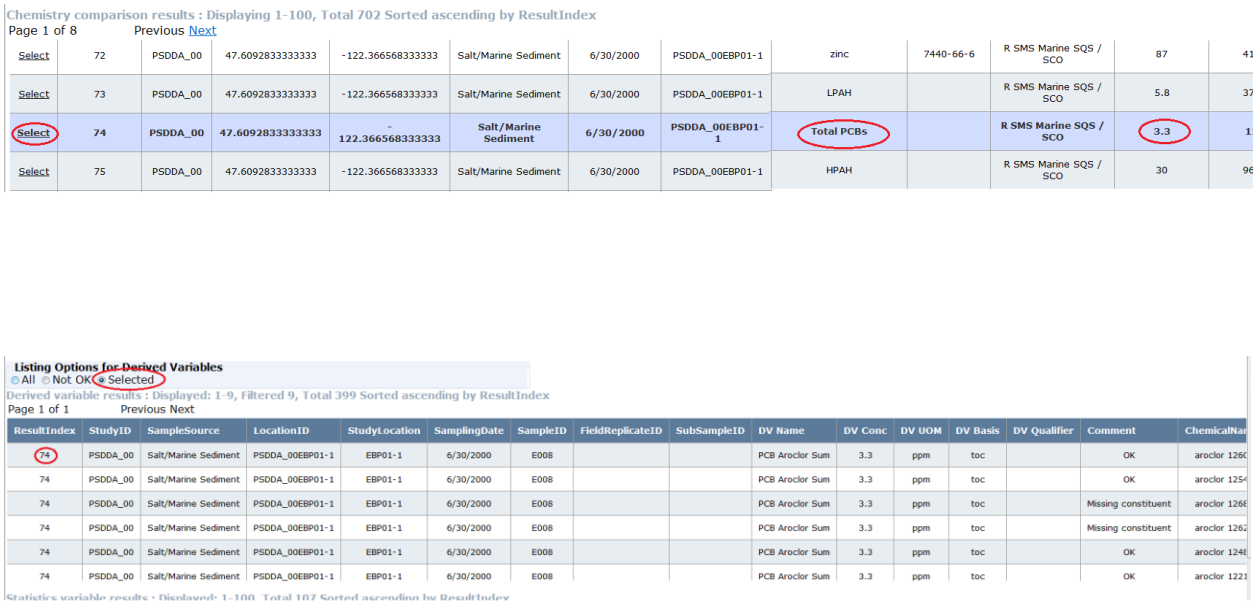
Some of the criteria in the system are defined using derived variables. Simple derived variables are calculated using the logic described in Appendix F. TEQ weighted derived variables are calculated using the logic described in Appendix G. Calculated values of derived variables are used for comparing to criteria values where ever possible. If derived variable calculation was not possible for any reason and reported values of derived variable reported values are available in query data, MyEIM uses reported derived variable values for comparison.

Derived Variable Results Grid

In cases where derived variables are calculated, the details of individual chemical constituents (from the top list) are listed in the middle derived variables grid. For example, if a criteria constituent of PCB is analyzed against a result containing PCB, the upper grid will display the summary of the evaluated concentration. The middle grid will contain 7 rows of data related to the result row in the upper grid because the PCB derived variable is defined with 7 constituents.

Figure 11a - Filtering of Derived Variables

Filtering of the Derived Variable grid is possible three ways. These options are available between the upper and lower grids in the Listing Options for Derived Variables. Selecting All will display all derived variable results. Not OK will only display those derived variable values where the evaluation of the constituents could not be performed as desired, this will be reflected in the comments. The final option is Selected. This will display only those derived variables that match the selected row in the upper grid as shown in Figure 11b. The first column in the upper grid provides the link to display details of a derived variable in the lower grid.



Chemistry comparison results : Displaying 1-100, Total 702 Sorted ascending by ResultIndex

Page 1 of 8 Previous Next

Select	72	PSDDA_00	47.6092833333333	-122.366568333333	Salt/Marine Sediment	6/30/2000	PSDDA_00EBP01-1	zinc	7440-66-6	R SMS Marine SQS / SCO	87	41
Select	73	PSDDA_00	47.6092833333333	-122.366568333333	Salt/Marine Sediment	6/30/2000	PSDDA_00EBP01-1	LPAH		R SMS Marine SQS / SCO	5.8	37
Select	74	PSDDA_00	47.6092833333333	-122.366568333333	Salt/Marine Sediment	6/30/2000	PSDDA_00EBP01-1	Total PCBs		R SMS Marine SQS / SCO	3.3	1
Select	75	PSDDA_00	47.6092833333333	-122.366568333333	Salt/Marine Sediment	6/30/2000	PSDDA_00EBP01-1	HPAH		R SMS Marine SQS / SCO	30	96

Listing Options for Derived Variables

All Not OK Selected

Derived variable results : Displayed: 1-9, Filtered 9, Total 399 Sorted ascending by ResultIndex

Page 1 of 1 Previous Next

ResultIndex	StudyID	SampleSource	LocationID	StudyLocation	SamplingDate	SampleID	FieldReplicateID	SubSampleID	DV Name	DV Conc	DV UOM	DV Basis	DV Qualifier	Comment	ChemicalNa
74	PSDDA_00	Salt/Marine Sediment	PSDDA_00EBP01-1	EBP01-1	6/30/2000	E008			PCB Aroclor Sum	3.3	ppm	toc		OK	aroclor 1260
74	PSDDA_00	Salt/Marine Sediment	PSDDA_00EBP01-1	EBP01-1	6/30/2000	E008			PCB Aroclor Sum	3.3	ppm	toc		OK	aroclor 1254
74	PSDDA_00	Salt/Marine Sediment	PSDDA_00EBP01-1	EBP01-1	6/30/2000	E008			PCB Aroclor Sum	3.3	ppm	toc		Missing constituent	aroclor 1268
74	PSDDA_00	Salt/Marine Sediment	PSDDA_00EBP01-1	EBP01-1	6/30/2000	E008			PCB Aroclor Sum	3.3	ppm	toc		Missing constituent	aroclor 1262
74	PSDDA_00	Salt/Marine Sediment	PSDDA_00EBP01-1	EBP01-1	6/30/2000	E008			PCB Aroclor Sum	3.3	ppm	toc		OK	aroclor 1248
74	PSDDA_00	Salt/Marine Sediment	PSDDA_00EBP01-1	EBP01-1	6/30/2000	E008			PCB Aroclor Sum	3.3	ppm	toc		OK	aroclor 1221

Statistics variable results : Displayed: 1-100, Total 107 Sorted ascending by ResultIndex

Figure 11b – Selected Total PCBs Derived Variables

Note: Derived variables are calculated only when defined in selected criteria. Derived variable calculation details are shown only when derived variables are calculated. They are calculated after data reduction at laboratory replicate level. At field replicate level aggregation Derived Variables grid will be empty since derived variables are already calculated at lab rep level and are only data reduced.

COMPARISON RESULT GRID COLUMNS

	ResultIndex	StudyID	Latitude	Longitude	SampleSource	SamplingDate	LocationID
Select	1	PSDDA_00	47.5889033333333	-122.362766666667	Salt/Marine Sediment	7/6/2000	PSDDA_00EBB01-1
Select	2	PSDDA_00	47.5889033333333	-122.362766666667	Salt/Marine Sediment	7/6/2000	PSDDA_00EBB01-1
Select	3	PSDDA_00	47.5889033333333	-122.362766666667	Salt/Marine Sediment	7/6/2000	PSDDA_00EBB01-1
Select	4	PSDDA_00	47.5889033333333	-122.362766666667	Salt/Marine Sediment	7/6/2000	PSDDA_00EBB01-1

Figure 12a – First few columns of the comparison results grid with lab replicate level data reduction.

First few columns of comparison grid are shown in Figure 12a. The first column has all cells labeled “select”. This is provides the link between the two grids. If the row contains a derived variable, clicking “select” on this row will filter the details of the derived variable and show it in the second grid. If the row is not a derived variable, then it will show an indicating message. Result Index column shows a unique identifier assigned for that row. This identifier is used to link this row for a derived variable detailed in the lower grid. By default this grid is sorted by Result Index column. All the other columns are reported values obtained from your custom search that identify the field replicates.

Note the sample Id column for analysis at lab replicate level. In some cases, field replicates of the same sample are assigned different sample Ids. On data reduction at field replicate level of those samples, the sample IDs of field replicates are concatenated and shown under sample IDs column as shown in Figure 12b.

Chemistry comparison results : Displaying 601-700, Total 701 Sorted ascending by ResultIndex

Page 7 of 8 Previous Next

	ResultIndex	StudyID	Latitude	Longitude	SampleSource	SamplingDate	LocationID	Replicates	UpperDepth	LowerDepth	DepthUOM	StudyLocation	SampleIDs
Select	601	PSDDA_00	47.59483	-122.357066666667	Salt/Marine Sediment	6/29/2000	PSDDA_00EBS02	1	0	10	cm	EBS02	E002
Select	602	PSDDA_00	47.59483	-122.357066666667	Salt/Marine Sediment	6/29/2000	PSDDA_00EBS02	1	0	10	cm	EBS02	E002
Select	603	PSDDA_00	47.59483	-122.357066666667	Salt/Marine Sediment	6/29/2000	PSDDA_00EBS02	1	0	10	cm	EBS02	E002
t	610	PSDDA_00	47.59483	-122.357066666667	Salt/Marine Sediment	6/29/2000	PSDDA_00EBS02	1	0	10	cm	EBS02	E002
t	611	PSDDA_00	47.59483	-122.357066666667	Salt/Marine Sediment	6/29/2000	PSDDA_00EBS02	1	0	10	cm	EBS02	E002
t	612	PSDDA_00	47.601285	-122.351261666667	Salt/Marine Sediment	6/29/2000	PSDDA_00EBS04	1	0	16	cm	EBS04	E003+E004
t	613	PSDDA_00	47.601285	-122.351261666667	Salt/Marine Sediment	6/29/2000	PSDDA_00EBS04	1	0	16	cm	EBS04	E003+E004
t	614	PSDDA_00	47.601285	-122.351261666667	Salt/Marine Sediment	6/29/2000	PSDDA_00EBS04	1	0	16	cm	EBS04	E003+E004
t	615	PSDDA_00	47.601285	-122.351261666667	Salt/Marine Sediment	6/29/2000	PSDDA_00EBS04	1	0	16	cm	EBS04	E003+E004

Figure 12b – First few columns of the comparison results grid with field replicate level data reduction.

Figure 13 shows eight columns specific to each criteria comparison, Qualifier and Replicates columns evaluated from data reduction as well as related reported values of concentration, unit of measure and basis for each chemical.

Replicates	SampleID	ChemicalName	CASNumber	CriteriaName	ChemicalConc	CriteriaConc	CriteriaUOM	CriteriaBasis	Exceedance	HitOrNot	Comment	Qua
1	E010	2-methylphenol	95-48-7	R 1988 Marine SQS / SCO Dry	20	63	ppb	dry	0.3175		OK	
1	E010	4-methylphenol	106-44-5	R 1988 Marine SQS / SCO Dry	44	670	ppb	dry	0.06567		OK	
1	E010	pentachlorophenol	87-86-5	R 1988 Marine SQS / SCO Dry	98	360	ppb	dry	0.2722		OK	
1	E010	phenanthrene	85-01-8	R 1988 Marine SQS / SCO	70	1500	ppb	dry	0.04667		OK	

Figure 13 – Criteria comparison columns of the comparison results grid.

Chemical Conc column shows concentration value after normalizing with respect to measurement basis and unit of measure of the selected chemical criteria.

Criteria Name, Criteria Conc, Criteria UOM and Criteria Basis column values are imported from chosen criteria for chemicals in each row.

Exceedance is the ratio of Chemical Conc to Criteria Value.

HitOrNot column indicates if Chemical Conc is greater than the Criteria Value.

Comment column displays a message giving an explanation in case the calculation was unsuccessful or any non-default feature was used. In case this is a derived variable, the details of derived variable calculation comments are also imported here.

Replicates column shows the number of replicates used in the process of data reduction.

Columns list continues as shown in Figure -14a and Figure – 14b.

Qualifier column displays qualifier code assigned to the chemical concentration after data reduction following the Qualifier Code Assignment business rule in Appendix E.

The TOC column shows an average of all % TOC values reported under lab or field replicate data aggregation or individually reported % TOC if the sample has no lab or/and field replicates . For TOC value to be displayed it is important to ensure the TOC data is queried as a part of the search data.

Reported Conc column shows data reduced concentration value based on the data reduction rule chosen in Preferences.

Reported UOM column shows unit of measure reported to the EIM and associated with data reduced concentration.

Reported Basis column shows the reported measurement basis for the chemical concentration reported to the EIM.

In case of no data reduction, Reported Conc, Reported UOM, and Reported Basis columns show reported values for Result Value, Result Value Units and result Basis from the EIM data search. Reporting Limit, RL Type, Detection Limit, and DL show reported values for Result Reporting

Limit, Result Reporting Limit Type, Result Detection Limit, and Result Detection Limit Type from the EIM data search.

Qualifier	TOC	ReportedConc	ReportedUOM	ReportedBasis	ReportingLimit	RLType	DetectionLimit	DLType	ReportedComment	AnalysisMethod
U	2.2	20	ppb	dry					U	UNKNOWN-SQ
	2.2	44	ppb	dry						UNKNOWN-SQ
U	2.2	98	ppb	dry					U	UNKNOWN-SQ
	2.2	70	ppb	dry						UNKNOWN-SQ

Figure 14a – Criteria comparison middle columns of the comparison results grid.

AnalysisMethod	AnalysisLab	ValidationLevel	GeoLocation	QAPlanning	Assessment	Contact	Program	Location Setting	Study Type	StudyName
UNKNOWN-SQ	Unknown - legacy data from SEDQUAL sediments database	QA1	78660547	4	See Results	Vu, Tuan	DMMP	Subtidal	SedDisposalSiteMonitor	Elliott Bay Full Monitoring
UNKNOWN-SQ	Unknown - legacy data from SEDQUAL sediments database	QA1	78660547	4	See Results	Vu, Tuan	DMMP	Subtidal	SedDisposalSiteMonitor	Elliott Bay Full Monitoring
UNKNOWN-SQ	Unknown - legacy data from SEDQUAL sediments database	QA1	78660547	4	See Results	Vu, Tuan	DMMP	Subtidal	SedDisposalSiteMonitor	Elliott Bay Full Monitoring
UNKNOWN-SQ	Unknown - legacy data from SEDQUAL	QA1	78660547	4	See Results	Vu, Tuan	DMMP	Subtidal	SedDisposalSiteMonitor	Elliott Bay Full

Figure 14b – Criteria comparison right most columns of the comparison results grid.

Analysis Method, Analysis Lab, and Validation Level show reported values for Result Method, Result Lab Name, and Result Validation Level from the EIM data search.

QA Planning, Assessment, Contact, Program, Location Setting, Study Type, and Study Name show reported values for Study QA Planning Level, Study QA Assessment Level, Ecology Contact, Ecology Program or Other Responsible Entity, Location Setting, Study Type, and Study Name from the EIM data search.

DERIVED VARIABLE GRID COLUMNS

Derived Variable grid is displayed only when data reduction at laboratory level is chosen. First few columns as shown in Figure 15, are reported values obtained from your custom search that identify the sample at field replicate level.

ResultIndex	StudyID	SampleSource	LocationID	StudyLocation	SamplingDate	SampleID	FieldReplicateID	SubSampleID
73	PSDDA_00	Salt/Marine Sediment	PSDDA_00EBP01-1	EBP01-1	6/30/2000	E008		
73	PSDDA_00	Salt/Marine Sediment	PSDDA_00EBP01-1	EBP01-1	6/30/2000	E008		
73	PSDDA_00	Salt/Marine Sediment	PSDDA_00EBP01-1	EBP01-1	6/30/2000	E008		

Figure 15 –Few left most columns of the Derived Variable grid.

DV Name	DV Conc	DV UOM	DV Basis	DV Qualifier	Comment	ChemicalName	CASNumber	WeightedConc	% Contribution	TOC	DLSF	Weight
LPAH	5.75	ppm	toc		OK	naphthalene	91-20-3	0.95	0	2		1
LPAH	5.75	ppm	toc		OK	acenaphthylene	208-96-8	0.95	0	2		1
LPAH	5.75	ppm	toc		OK	acenaphthene	83-32-9	0.95	0	2		1

Figure 16 –Columns specific to calculation details of the Derived Variable.

DV Name, DV UOM and DV basis columns show the information from the criteria based on which derived variables are calculated.

Calculated concentration is shown in DV Conc column.

DV qualifier shows the code assigned to the calculated value based on the derived variable calculation logic (Please refer to appendices F and G).

Comment column indicates messages arising from calculation. ‘OK’ indicates that calculation is completed successfully, and no missing constituents.

For every derived variable there are as many rows as its constituent chemicals, one for each chemical. Chemical Name column indicates name of the constituent.

Weighted Conc shows the concentration of the chemical after normalizing with respect to unit of measure and measurement basis is necessary, and scaled by detection limit scaling factor (DLSF) if concentration is U (non-detect) qualified and scaled by weights as assigned in the definition of the derived variable in the criteria.

%Contribution column shows the contribution of this weighted concentration to the total sum that makes up derived variable concentration.

TOC is the average percent TOC value of the sample at laboratory replicate data aggregation level or the reported TOC value without laboratory/field replicates. For TOC normalization, it is important to ensure the TOC data is queried as a part of the search data.

Detection Limit Scaling Factor and weight for each chemical originate from the definition of the derived variable in the criteria.

ReportedConc	ReportedUOM	ReportedBasis	Reported Qualifier	ReportingLimit	RLType	DetectionLimit	DLType	ReportedComment	ValidationLevel	AnalysisMethod	AnalysisLab	UpperDepth	LowerDepth	DepthUOM
19	ppb	dry	U					U	QA1	UNKNOWN-SQ	Unknown - legacy data from SEDQUAL sediments database	0	16	cm
19	ppb	dry	U					U	QA1	UNKNOWN-SQ	Unknown - legacy data from SEDQUAL sediments database	0	16	cm
19	ppb	dry	U					U	QA1	UNKNOWN-SQ	Unknown - legacy data from SEDQUAL sediments database	0	16	cm

Figure 17a – Columns specific to reported values of the chemical, sample and sampling depth.

AnalysisMethod	AnalysisLab	UpperDepth	LowerDepth	DepthUOM	Latitude	Longitude	GeoLocation	Study Type	Location Setting	QAPlanning	Assessment	Contact	Program	StudyName
UNKNOWN-SQ	Unknown - legacy data from SEDQUAL sediments database	0	16	cm	47.6092833333333	-122.366568333333	29813000	SedDisposalSiteMonitor	Subtidal	4	See Results	Vu, Tuan	DMMP	Elliott Bay Full Monitoring
UNKNOWN-SQ	Unknown - legacy data from SEDQUAL sediments database	0	16	cm	47.6092833333333	-122.366568333333	29813000	SedDisposalSiteMonitor	Subtidal	4	See Results	Vu, Tuan	DMMP	Elliott Bay Full Monitoring
UNKNOWN-SQ	Unknown - legacy data from SEDQUAL sediments database	0	16	cm	47.6092833333333	-122.366568333333	29813000	SedDisposalSiteMonitor	Subtidal	4	See Results	Vu, Tuan	DMMP	Elliott Bay Full Monitoring

Figure 17b –Right most columns of the Derived Variable grid.

Figures 17a and 17b shows the remaining columns of the derived variables grid.

Reported Conc shows the data reduced value of the chemical concentration, if the laboratory or field replicate results are reported. Otherwise Reported Conc originate from search results.

Reported UOM and Reported basis originate from search results.

Reported Qualifier is the qualifier code arising from data reduction or reported value.

Three depth columns are related to sediment sample identity and the Lat/Long, GeoLocation, and Location Setting column values identify the location.

QA Planning, Assessment, Contact, Program, and Study Name show reported values for Study QA Planning Level, Study QA Assessment Level, Ecology Contact, Ecology Program or Other Responsible Entity, and Study Name from the search results.

EXERCISE 2: MAP RESULTS

The analyzed results can be mapped to show where chemical concentrations exceeded the selected Comparison Criteria. This is done by clicking the Map Results link.

(1) Click on "Map Results".

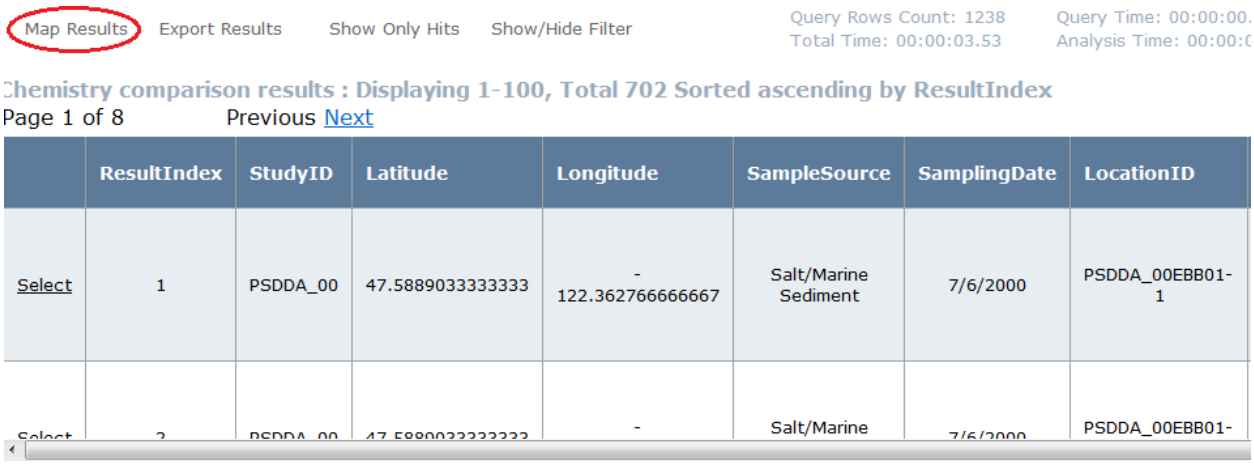


Figure 18 –Map Results link on Analysis Results Page

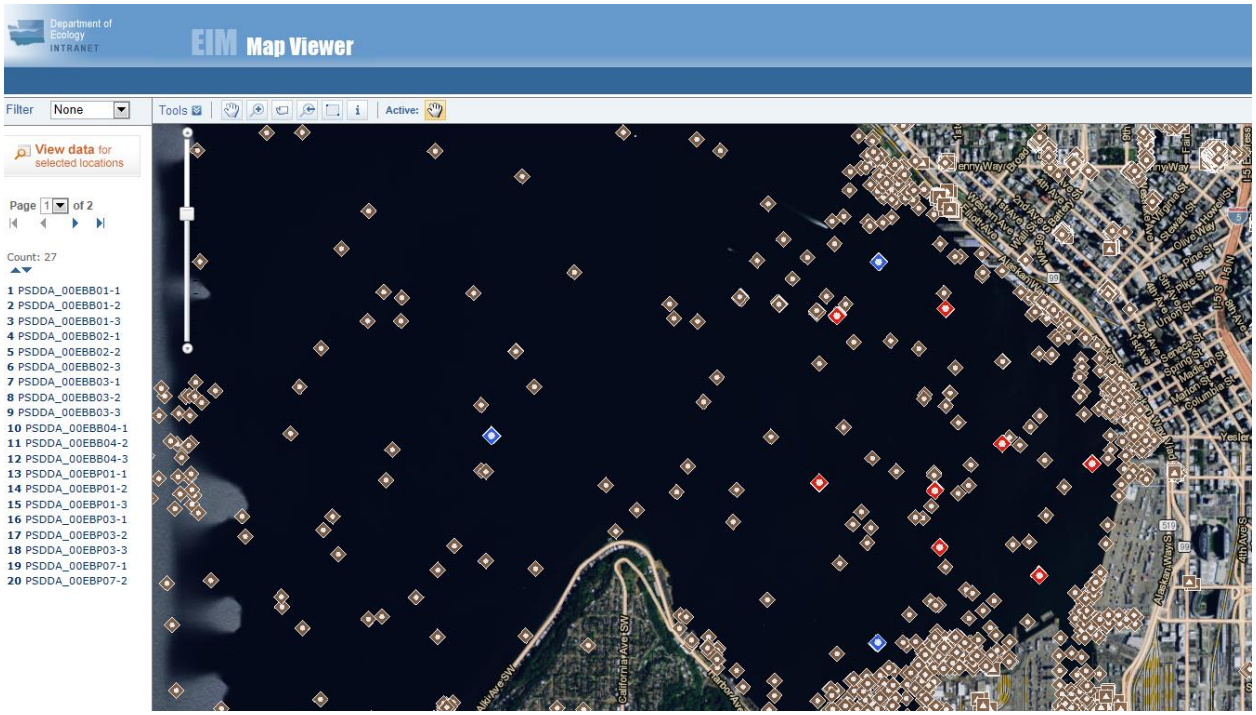


Figure 19 - Mapped analysis results for User Study ID = PSDDA_00

When results are mapped, concentration values from samples taken which exceed the concentration value of a selected standard, the resulting dot on the map is automatically highlighted in Red.

EXERCISE 3: EXPORT RESULTS

Selecting the Export Results link will allow you to download the analyzed results as a CSV file. This file can then be opened in a spreadsheet program such as Microsoft Excel.

(1) Click on the Export Results link on the Analysis Results page.

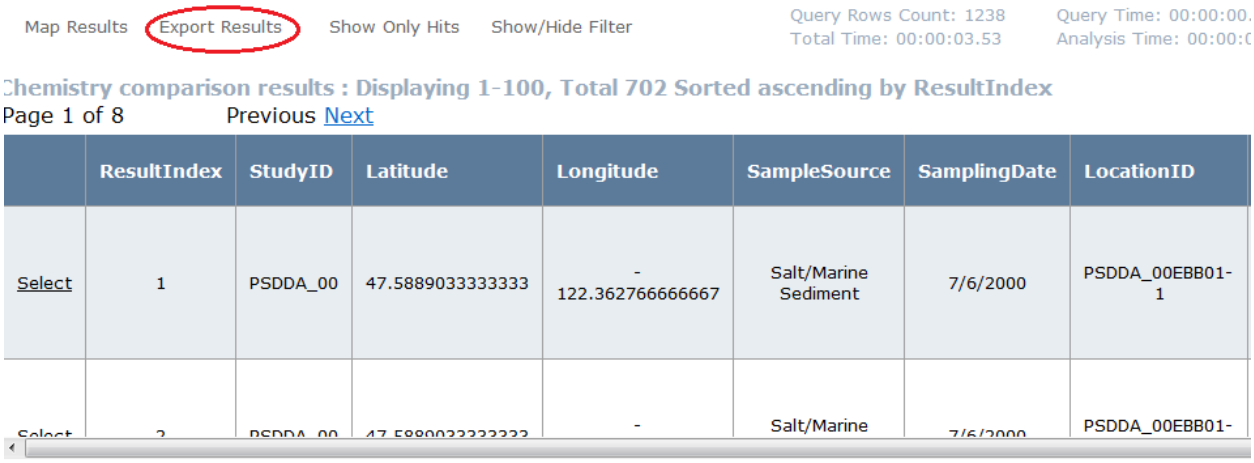


Figure 20 - Export Results link on Analysis Results Page

(2) A dialog box prompt will confirm the file download. Click Open in Figure 21a to bring you to the zip file in Figure 21b. This zip file will contain two spreadsheet files, chemistry comparison results at the top grid and derived variable results at the middle grid on Analysis Results page.

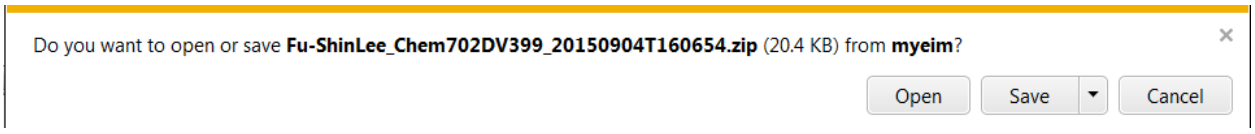


Figure 21a - Export results dialog box.

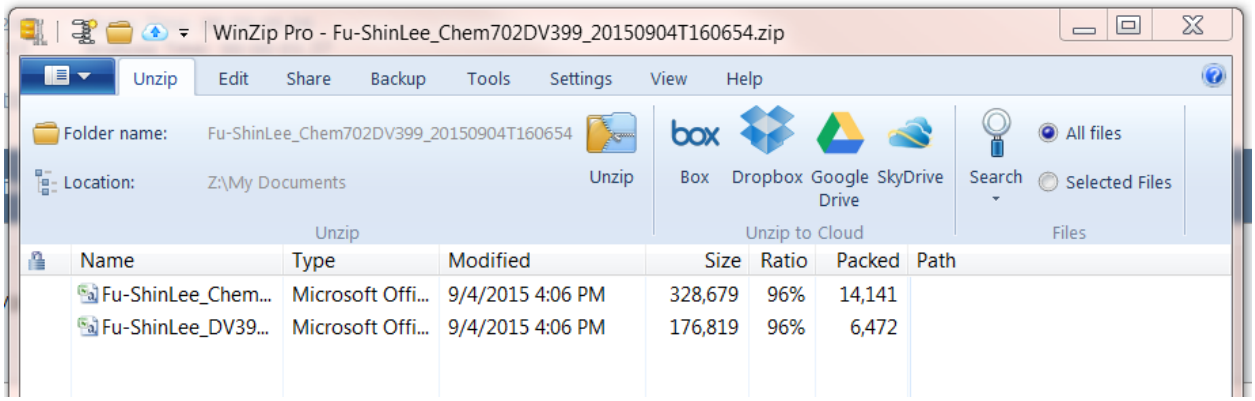


Figure 21b - Export results in Zip File.

You can double click on the files in Figure 21b to view and save these spreadsheets in your folder.

EXERCISE 4: SHOW ONLY HITS

The Show Only Hits link on Analysis Results Page will filter the Comparison Results grid to show only those chemicals that exceed the selected standards.

(1) Click on the Show Only Hits link.

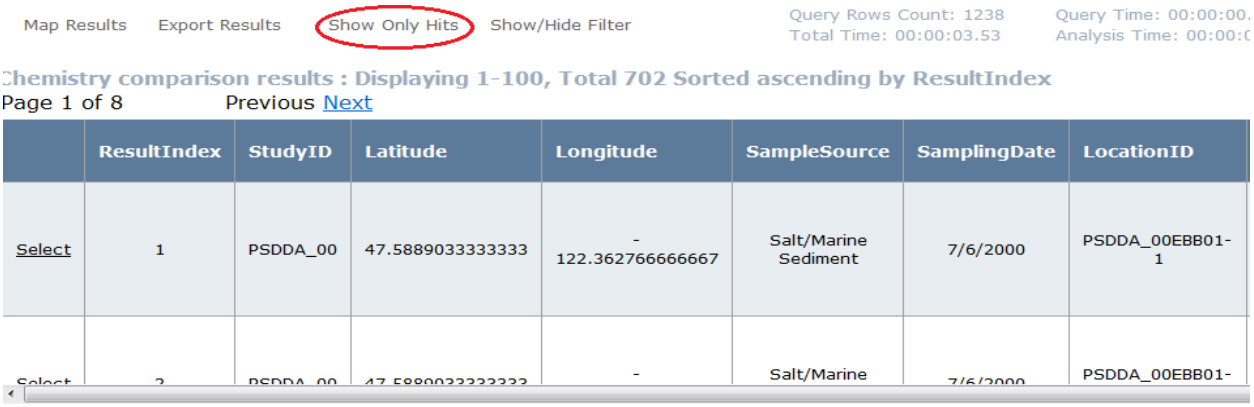


Figure 22 - Show Only Hits link on Analysis Results Page

(2) Notice that only the chemicals exceeding the standard are displayed.

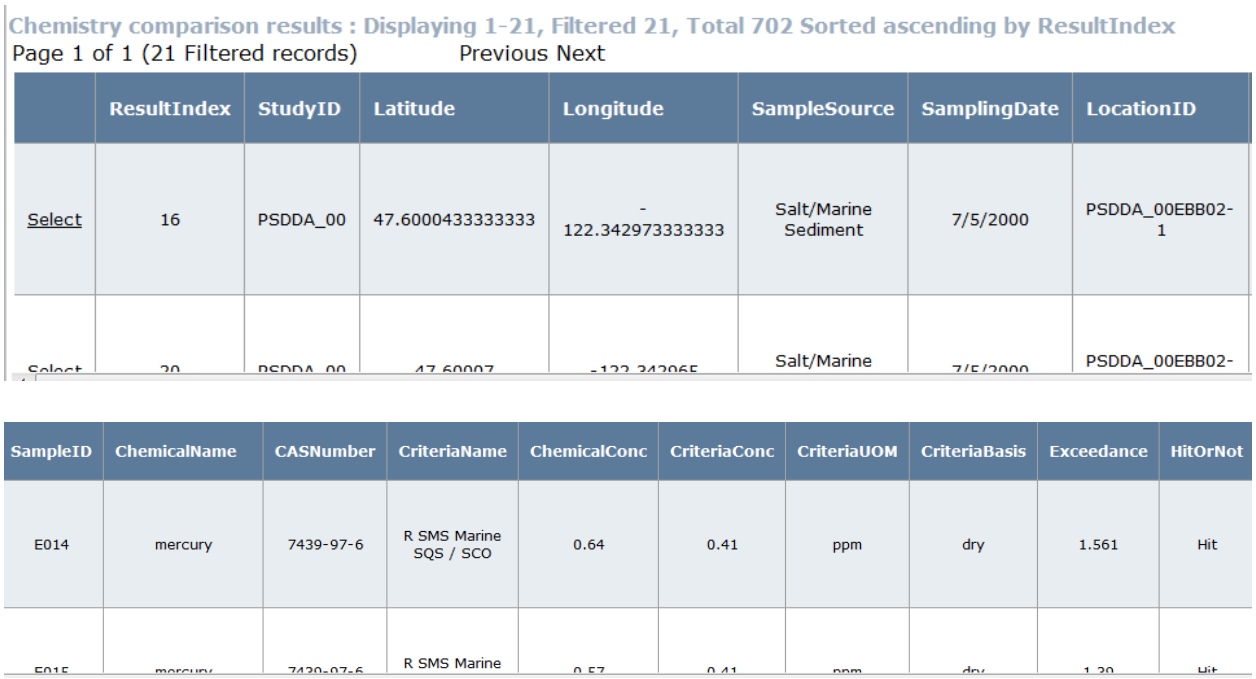


Figure 23 - Result data exceeding the standard.

EXERCISE 5: SHOW/HIDE FILTER

Selecting the Show/Hide Filter link will allow you place filtering constraints on the analyzed data you are viewing. Previous exercise in fact processed a predefined filter to look for hits.

(1) Click on the Show/Hide Filter link.

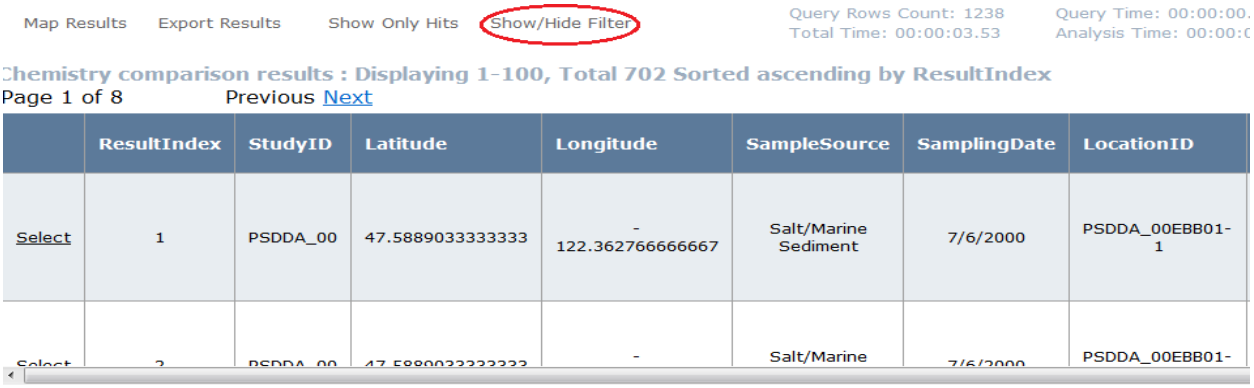


Figure 24 - Show/Hide filter link

(2)The filter appears in Figure 25. The Filter control allows you to set constraints on the results in the grid.

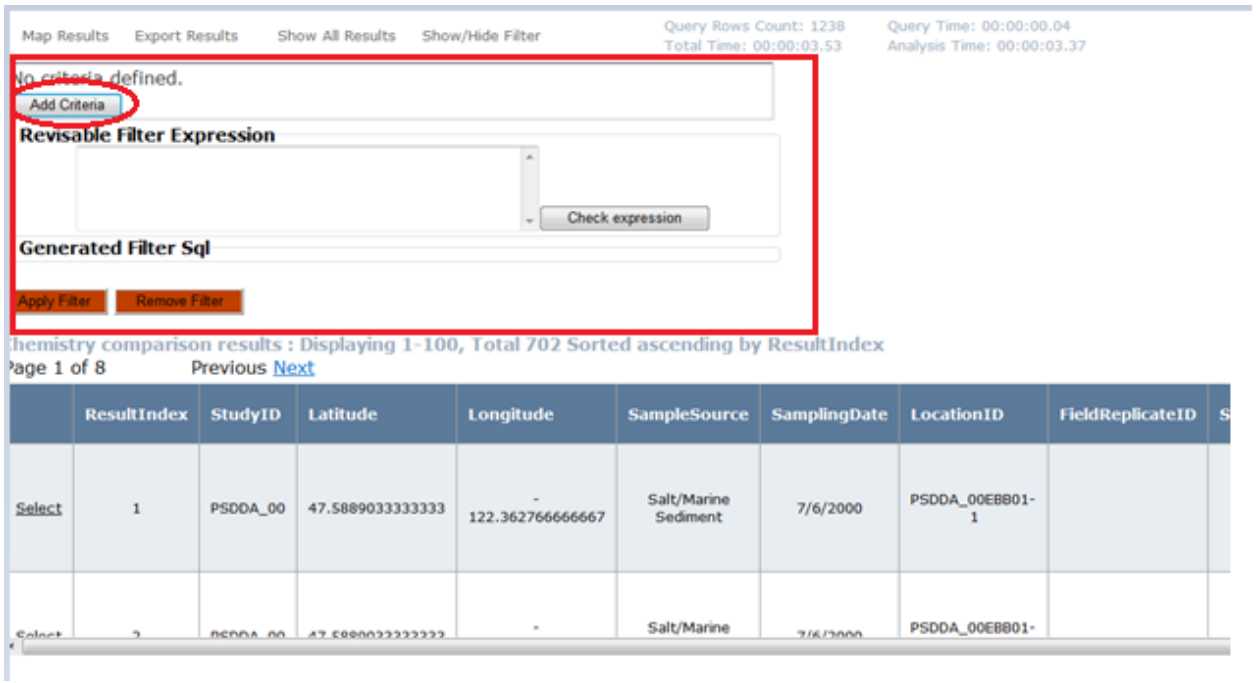


Figure 25 - Filter control becomes visible above the comparison results.

The filter control used here works just like the Custom Search filter control. To begin, click on the 'Add Criteria' button. A new filter row will be displayed.

(3) Select the column name you wish to filter on from the "Field Name" drop list in Figure 26.

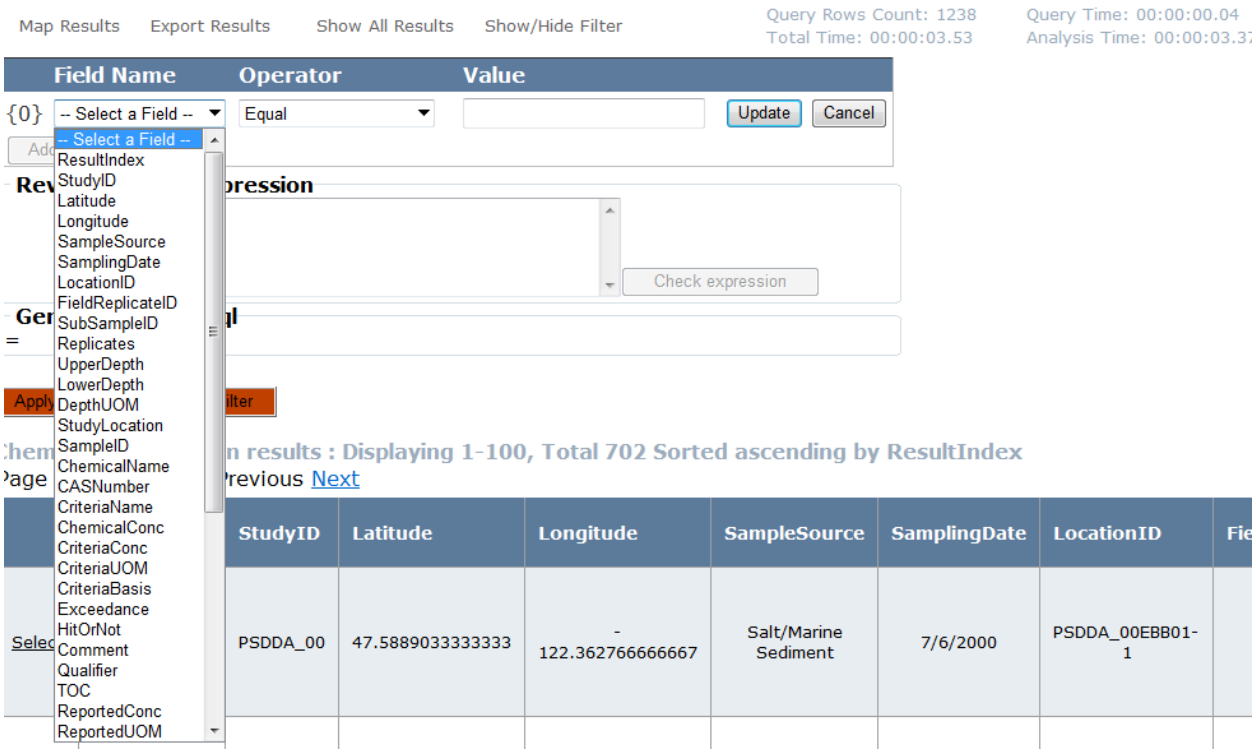


Figure 26 – The Custom Filter Control

(4) Next select the operator.

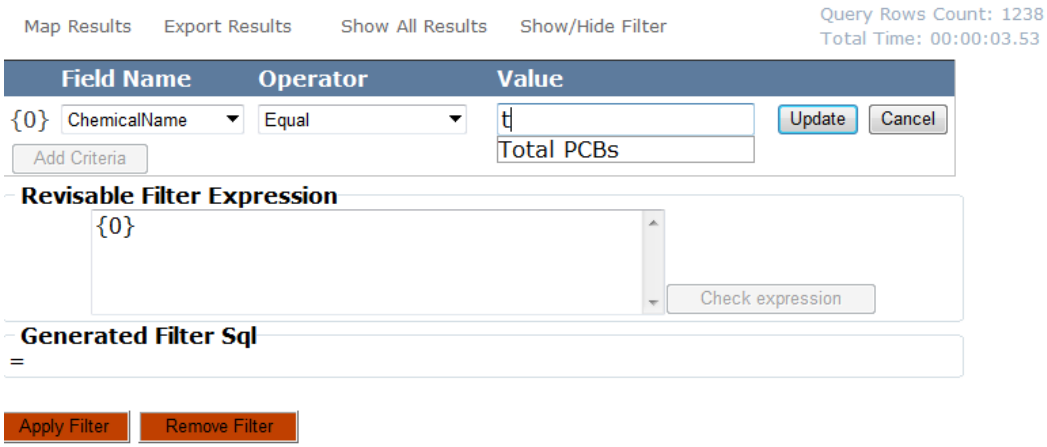


Figure 27 – The Custom Filter Control: select an operator and input a value.

(5) Finally, enter the value for the filter and click the Update button in Figure 27.

(6) Click the Apply Filter button to limit the displayed result to only those that match the filter you created.

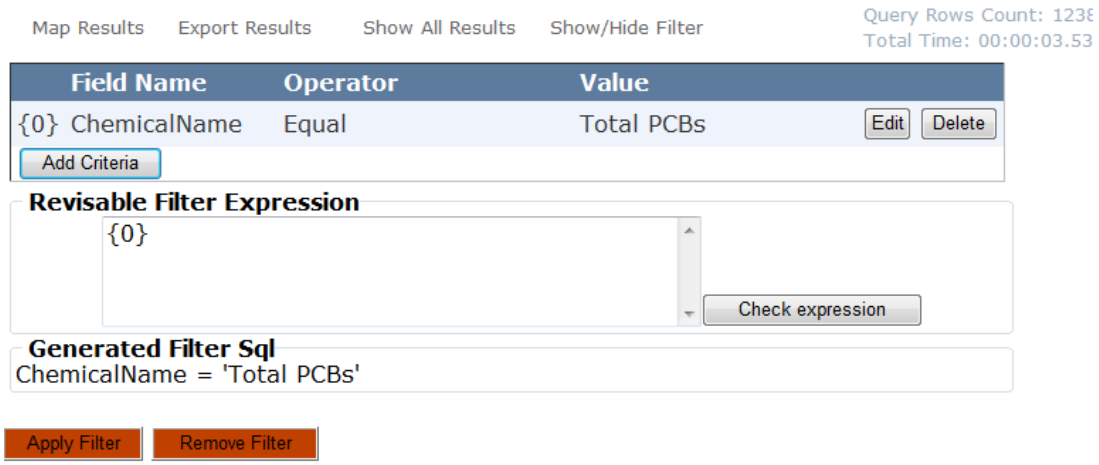


Figure 28 – PSDDA_00 study run against the R SMS Marine SQS standard filtered to show only Total PCBs

Note: When you Export Results, the exported files will contain only the filtered results. When you Map Results only the filtered results show up in the Map.

The filter tool operates on the Chemistry Analysis results grid. The Derived Variable grid is filtered through the radio buttons shown in Listing Options for Derived Variables and using "select" link provided at the beginning of each row in the Chemistry Analysis results grid.

Results can be sorted based on column values in the chemistry results as well as derived variables grids by clicking on the column header which needed to be sorted. Sorting can be done with or without applying the filters. If the column values are associated with values in the other columns, MyEIM sorting algorithm takes this factor into account. For example, since concentrations are associated with unit of measure, MyEIM sorts concentrations by taking into account the unit of measure. Similarly upper depth and lower depth values are sorted using depth unit of measure.

Note: Sort and filter the output feature in MyEIM is especially useful if the sorted/filtered column is dependent on another column as in the above example. In Excel you will need to write a custom sorting/filtering macro or code to achieve the same result.

Chemistry comparison results : Displaying 1-16, Filtered 16, Total 702 Sorted ascending by ResultIndex

Page 1 of 1 (16 Filtered records) Previous Next

	ResultIndex	StudyID	Latitude	Longitude	SampleSource	SamplingDate	LocationID
Select	74	PSDDA_00	47.6092833333333	-122.366568333333	Salt/Marine Sediment	6/30/2000	PSDDA_00EBP01-1

SampleID	ChemicalName	CASNumber	CriteriaName	ChemicalConc	CriteriaConc	CriteriaUOM	CriteriaBasis	Exceedance	HitOrNot
E008	Total PCBs		R SMS Marine SQS / SCO	3.3	12	ppm	toc	0.275	

Figure 29 – Sorting analyzed results. MyEIM sorting algorithm takes into account associated column values.

CUSTOMIZING MY ANALYSIS

Eventually, you may want to define cleanup criteria of your own with chemicals and criteria values different from those found in the Standard Cleanup Criteria list. MyEIM analysis allows you to create “User Defined Cleanup Criteria” by either copying existing standard criteria or, by creating new criteria.

If you copy existing criteria you can always alter it. If you defined new criteria, you can add constituents to it. You can delete or modify each of the constituents. There are three types of constituents: chemicals, derived variables and user defined derived variables.

Complete lists of chemicals and standard derived variables are already available in MyEIM for you to choose from. You can define your own customized derived variables and add them to criteria list. In this section we shall create user defined criteria and user defined derived variables.

EXERCISE 6: CREATING CUSTOM CLEANUP CRITERIA BY ALTERING A COPY

(1) From the Choose Comparison Criteria page, select the User Defined Cleanup Criteria tab. If this is the first time you've clicked this tab, a message informs you to "Please make a copy of the Standard Cleanup Criteria that you want to see in this tab or Add a new one...." Notice how no criteria are listed.

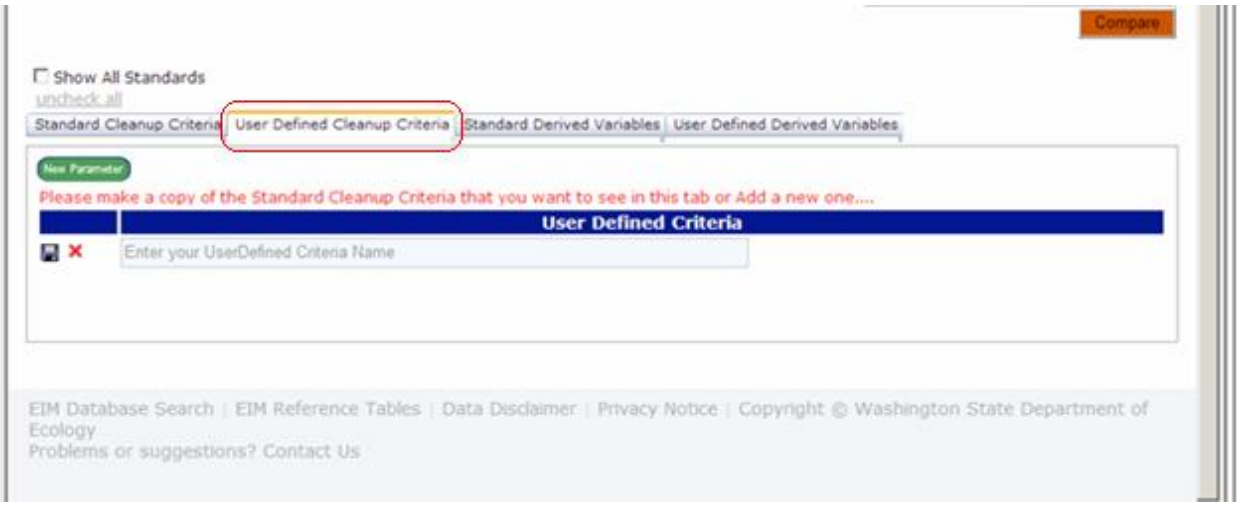


Figure 30 - Empty User Defined Cleanup Criteria

Go back to the first Cleanup Criteria tab. To the right of each list item is a Copy button . Clicking the Copy button creates a copy of the definition under your profile for modification. Click the Copy image for "R SMS Marine SQS / SCO".

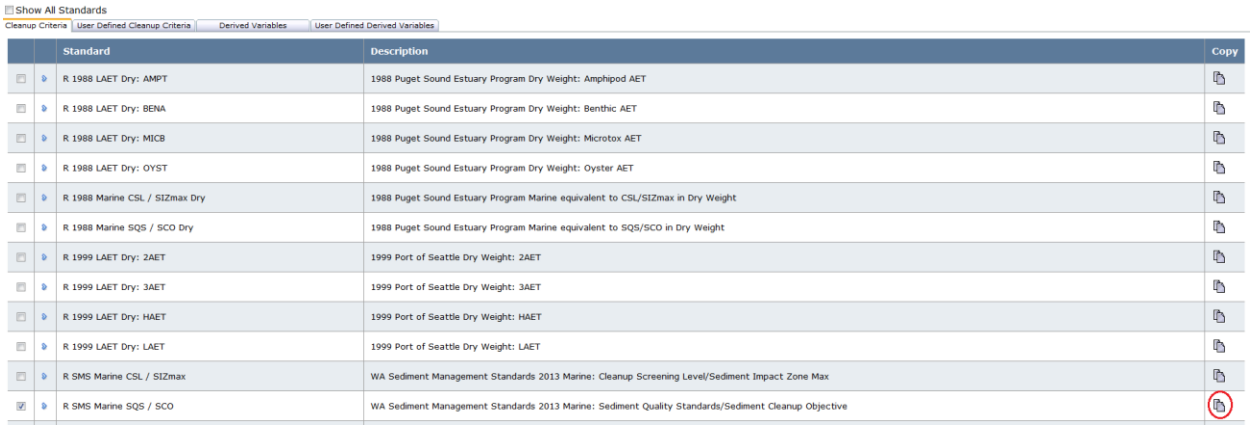


Figure 31 – The Copy Cleanup Criteria button

(2) After you click the Copy image button, the screen will automatically go to the User Defined Cleanup Criteria tab. You should now see an entry as shown below.

Figure 32 - This newly created User Defined Cleanup Criteria is a copy of R SMS Marine SQS

The new entry has three actions that you can perform. Each is represented by an icon. The blue arrow symbol highlights the item and displays its constituents.

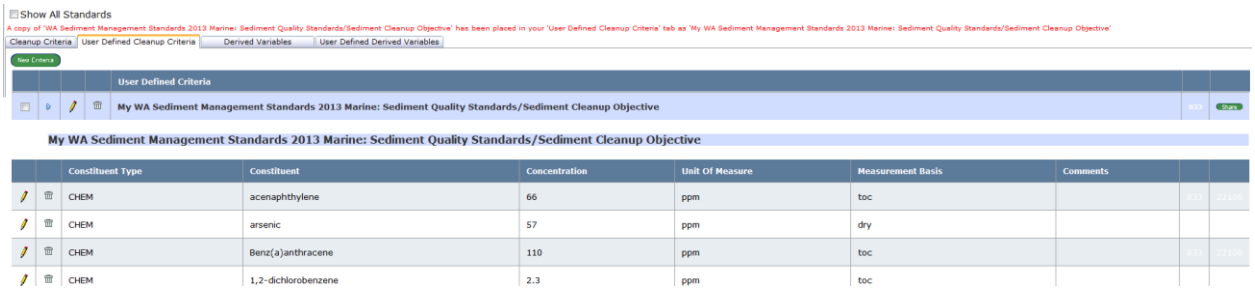


Figure 33 - User Defined cleanup criteria selected

(3)The name of the new user defined cleanup criteria can be modified by clicking the pencil icon. Change the name to something meaningful and click the disk icon to save. In this case the name was changed to "My 2015 Marine: Sediment Quality Standards/Sediment Cleanup Objective".

Figure 34 - User Defined Cleanup Criteria in Edit Mode

When a user defined criteria is selected, its constituents are listed in the grid below. Each constituent can be edited by clicking on the pencil image. The pencil image disappears and is replaced by a Save disk image and a Cancel red X image. You'll notice there is also a Delete trash can image. After making your change, be sure to select Save.

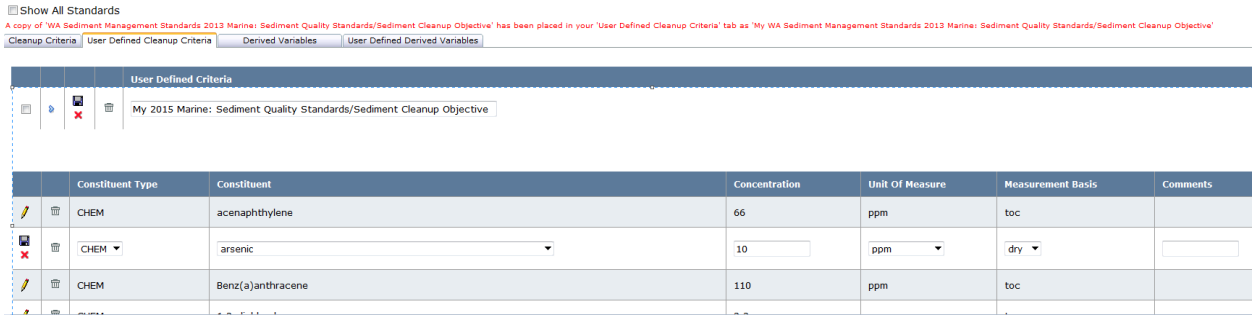


Figure 35 - User Defined Cleanup Criteria Constituent in Edit Mode

(4) Once you are satisfied with the constituent list, you can select this User Defined Cleanup Criteria.

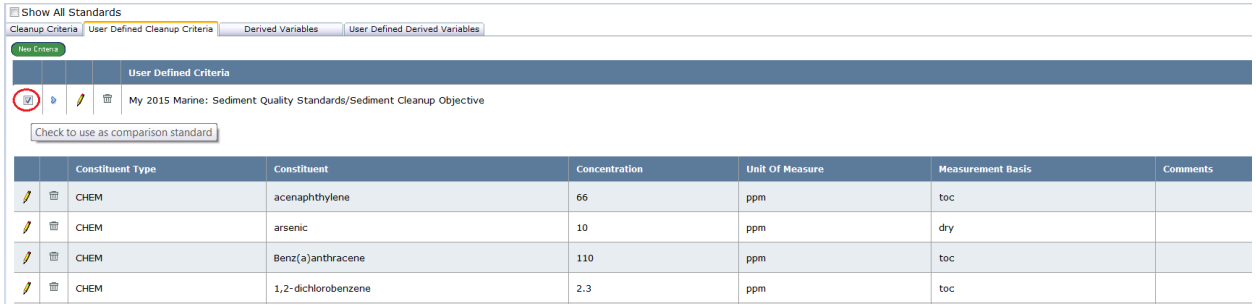


Figure 36 - User Defined Cleanup Criteria selected for comparison.

When you click Compare, your custom User Defined Cleanup Criteria will be used for analysis.

EXERCISE 7: CREATING A CUSTOM DERIVED VARIABLE

(1) Click the User Defined Derived Variables tab. A message instructs you to "Please make a copy of the Standard derived variable that you want to see in this tab…" and a blank user defined derived variable is open and waiting to be defined. Just like the Cleanup Criteria, you can either copy an existing derived variable and alter it, or create a new one from fresh.

(2) To Copy and alter an existing Derived Variable: Go to the Derived Variables tab. To the right of each list item is a Copy image  . Clicking the Copy button creates a copy of the definition under your profile for modification.

Figure 37- User Defined Derived Variables

(3) To Create a New Derived Variable: Click the green 'New D.V.' button in the User Defined Derived Variable tab if a new derived variable isn't already open. In the "UDDerivedVariable Name" column, simply enter a name for the new derived variable. Give it a "Detection Limit Scaling Factor" value, and optional comments. Click the disk icon to save.

Figure 38 - Empty User Defined Derived Variables

The Detection Limit Scaling Factor scales U qualified and/or non-detect reported values. If the constituent chemical is a non-detect, then its reported value will be normalized to the unit of measure, normalized to measurement basis if required, scaled down by detection limit scaling factor, multiplied by the toxicity equivalency factor and then added to the total derived Variable Value. Allowed value is in the range 0 <= 'Detection Limit Scaling Factor' <=1.

The new entry has three actions that you can perform. Each is represented by an icon. The name of the new User Defined Derived Variable can be modified by clicking the pencil icon. Change the name to something meaningful and click the Save icon. In this case the name was changed to "Polychlorinated Biphenyls High Weight".

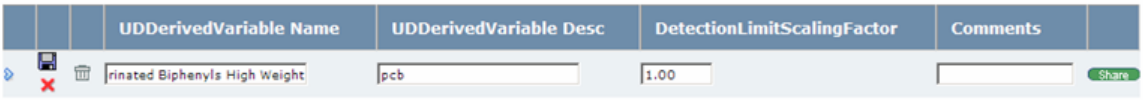


Figure 39 - User Defined Derived Variable in Edit Mode

(4) The blue arrow symbol selects the item and displays the constituents in a list. Clicking the green "New Constituent" button will open a new row in edit mode. Simply select a chemical from the drop-down list and assign a weight.

Figure 40 - Constituents listed for a user defined derived variable.

Each constituent can be edited by clicking on the pencil image. The pencil image disappears and is replaced by a Save disk image , a Cancel red X image, and a Delete trash can image .

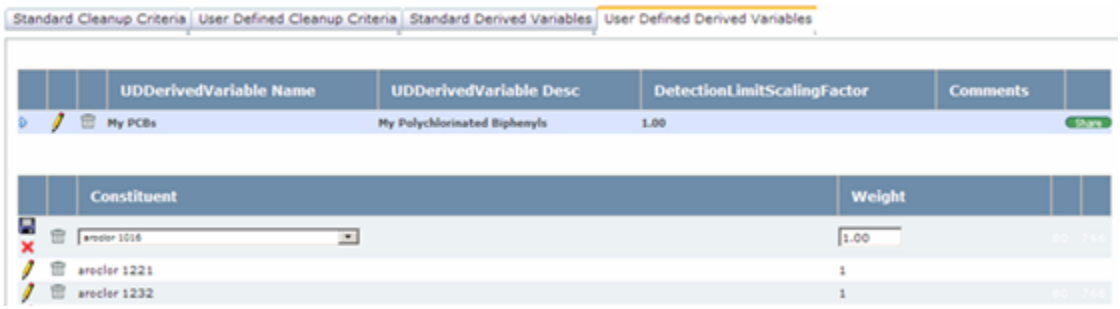


Figure 41 - Derived variable constituents in edit mode.

After making your change, select the Save or Cancel image to save or cancel your edit.

EXERCISE 8: ADDING A CUSTOM DERIVED VARIABLE TO A CUSTOM CRITERION

You will need to add the derived variable you defined in the previous exercise in order to calculate it and compare to a criteria value of your own.

(1) To use your custom derived variable in analysis, switch over to the User Defined Cleanup Criteria tab. Click the green "New Criteria" button and name the cleanup criteria as 'PCB test'.

(2) In the Constituent Type drop-down, select "UDDV" and then select the custom derived variable you just created from the constituent drop-down.

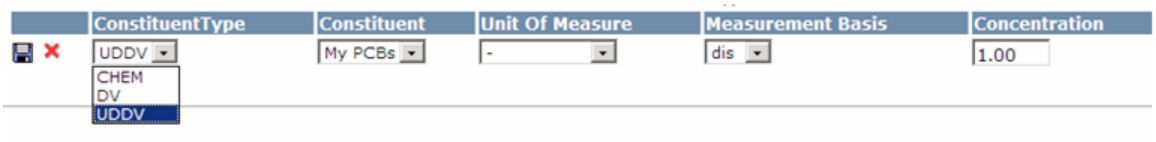


Figure 42 - Selecting a User Defined Derived Variable for a custom analysis.

Set the other properties (Unit of Measure, Measurement Basis, and Concentration) and then save the constituent.

(3)Then check the checkbox to the left of the cleanup criteria and click the orange "Compare" button.

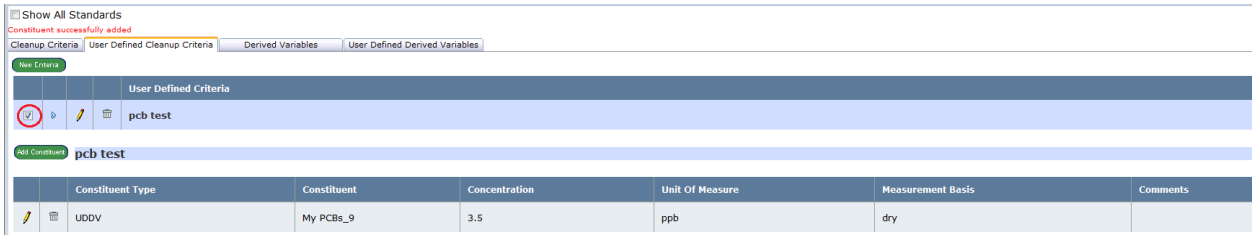


Figure 43 – Calculating custom derived variable and comparing to custom criterion.

(4) Your custom derived variable will be calculated and compared with your criteria concentration value.

Chapter 6: Bioassay Analysis

The MyEIM Bioassay Analysis application provides the tools to perform bioassay analysis on the searched bioassay results versus the selected bioassay standards.

OVERVIEW

The MyEIM Bioassay Analysis application provides tools to analyze bioassay sample data using selected standards. Users are not limited to comparison using predefined standards (also known as Standard Cleanup Criteria). MyEIM Bioassay Analysis also provides an interface for you to define your own set of standards (also known as User Defined Cleanup Criteria).

GETTING STARTED (BIOASSAY DATA SEARCH)

To begin the bioassay analysis process, you will need a result set from the quick start search template in Search Templates or your saved search in My Custom Search or bioassay search in Custom Search.

Note: If you need a sediment bioassay result set to get started, select 'Bioassay data check' in Search Templates of the Portal Page as shown in Figure 1. Clicking on 'Save As' will bring you to the Bioassay Search page. Clicking on 'Show Data' will bring you to the searched Bioassay Results page as shown in Figure 2.

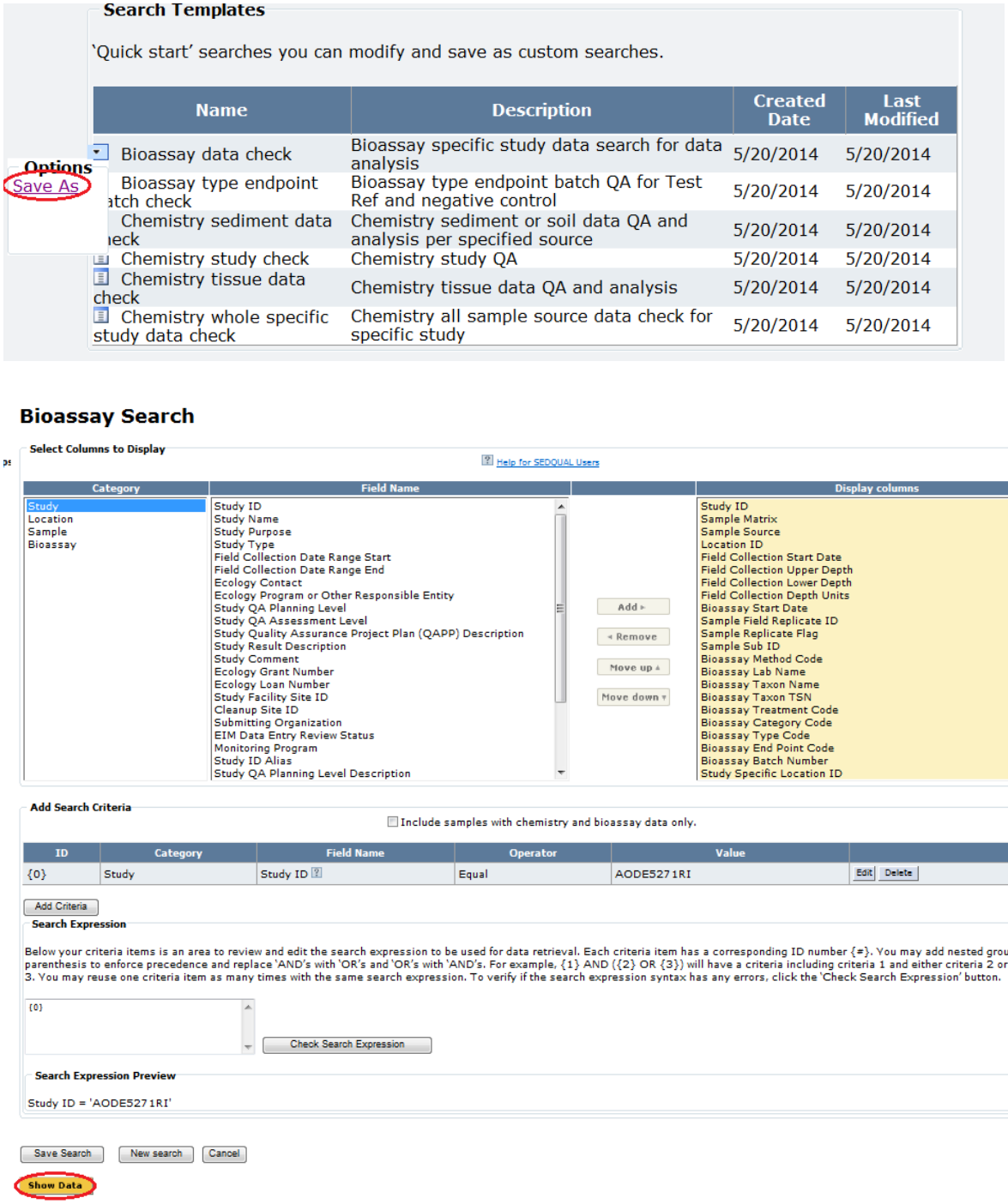


Figure 1 - Perform a quick bioassay search from MyEIM home and Bioassay Search pages.

On the Results page, click the 'Analyze Data' link in the upper left corner of the content page. This link will take you to the 'Bioassay Test Parameters' page of the Analysis application.

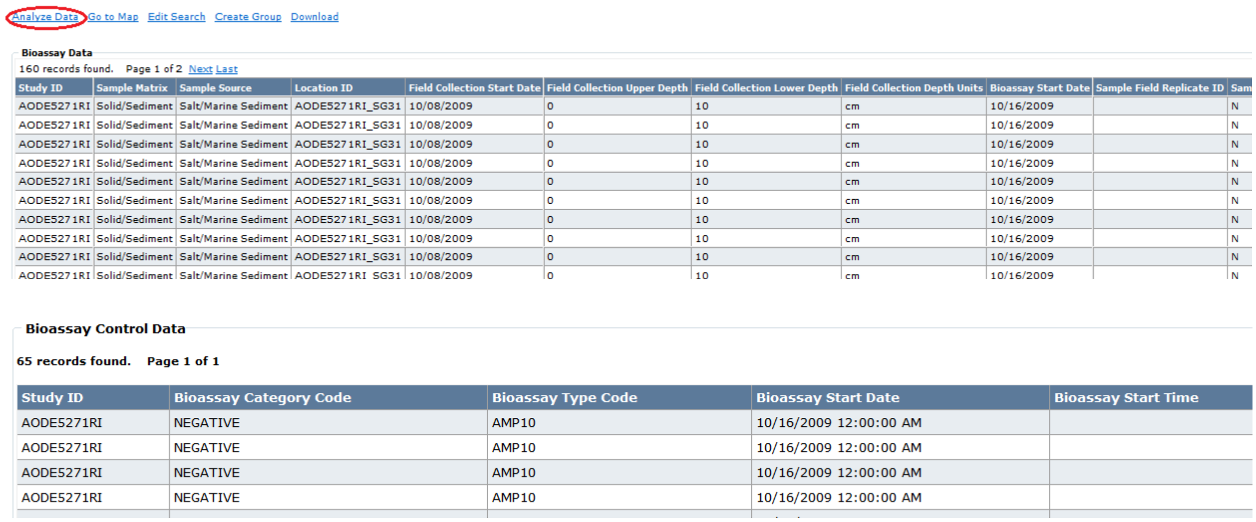


Figure 2 – My EIM Bioassay query results page – click on Analyze Data

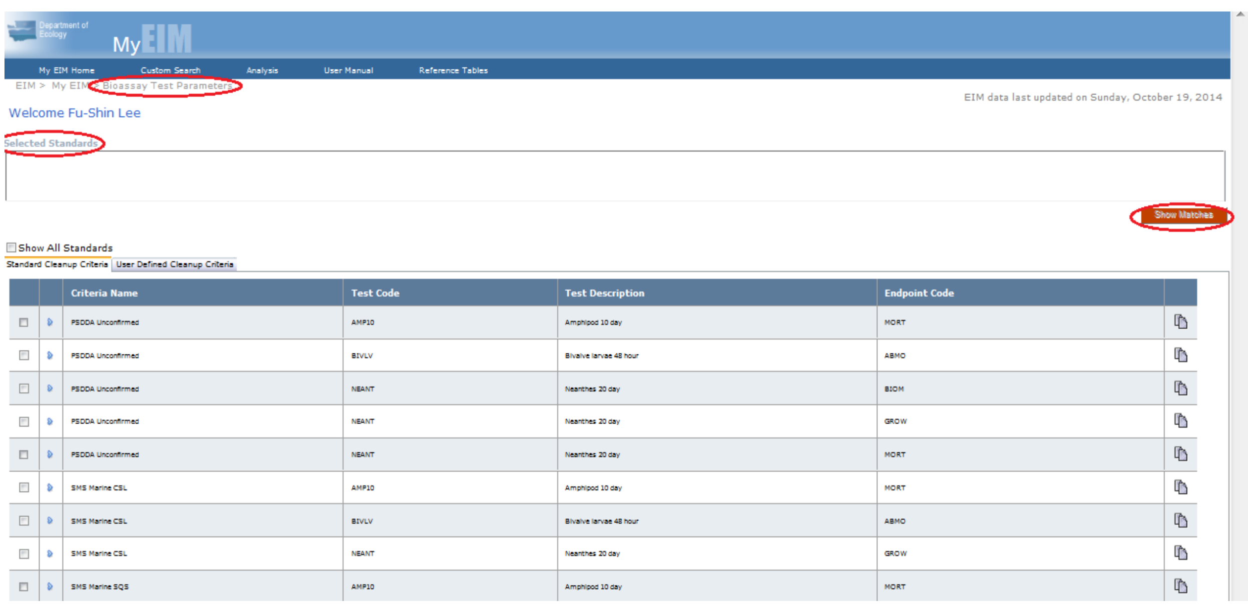


Figure 3 – Bioassay Test Parameters Page of MyEIM Bioassay Analysis

What happened to your data? Don't worry. Custom Search hands off the results to Analysis when you come into the Analysis application.

The first page of the Bioassay Analysis process is used to collect settings for the upcoming analysis. Notice, this page is similar to the chemical analysis page.

Below the welcome banner is the ‘Selected Standards’ list box. A prominent ‘Show Matches’ button is just below the Selected Standards box. The Show All Standards checkbox sits on top of the Criteria grid, organized by a set of page tabs.

Selected Standards

This list box will display the list of bioassay criteria which have been selected to use during analysis. Criteria are added and removed from this box through the check and uncheck of rows in the Criteria and Variables grid. You can select only one unique combination of EndPoint Code and Test Code.

Show Matches

Clicking this button will take you to the second step (Bioassay Match page in Figure 4) of the Bioassay Analysis process. The Selected Standards that have been chosen are used to match the Standard Test Code and Endpoint Code to the queried data’s Test Code and Endpoint Code of the Control and Reference bioassay data.

Compare

Clicking this button will take you to the Bioassay Summary page as shown in Figure 5. You can view detailed individual bioassay test sample results by clicking on the blue error

Export Results

Clicking this button will export all the bioassay summary results in spreadsheet.

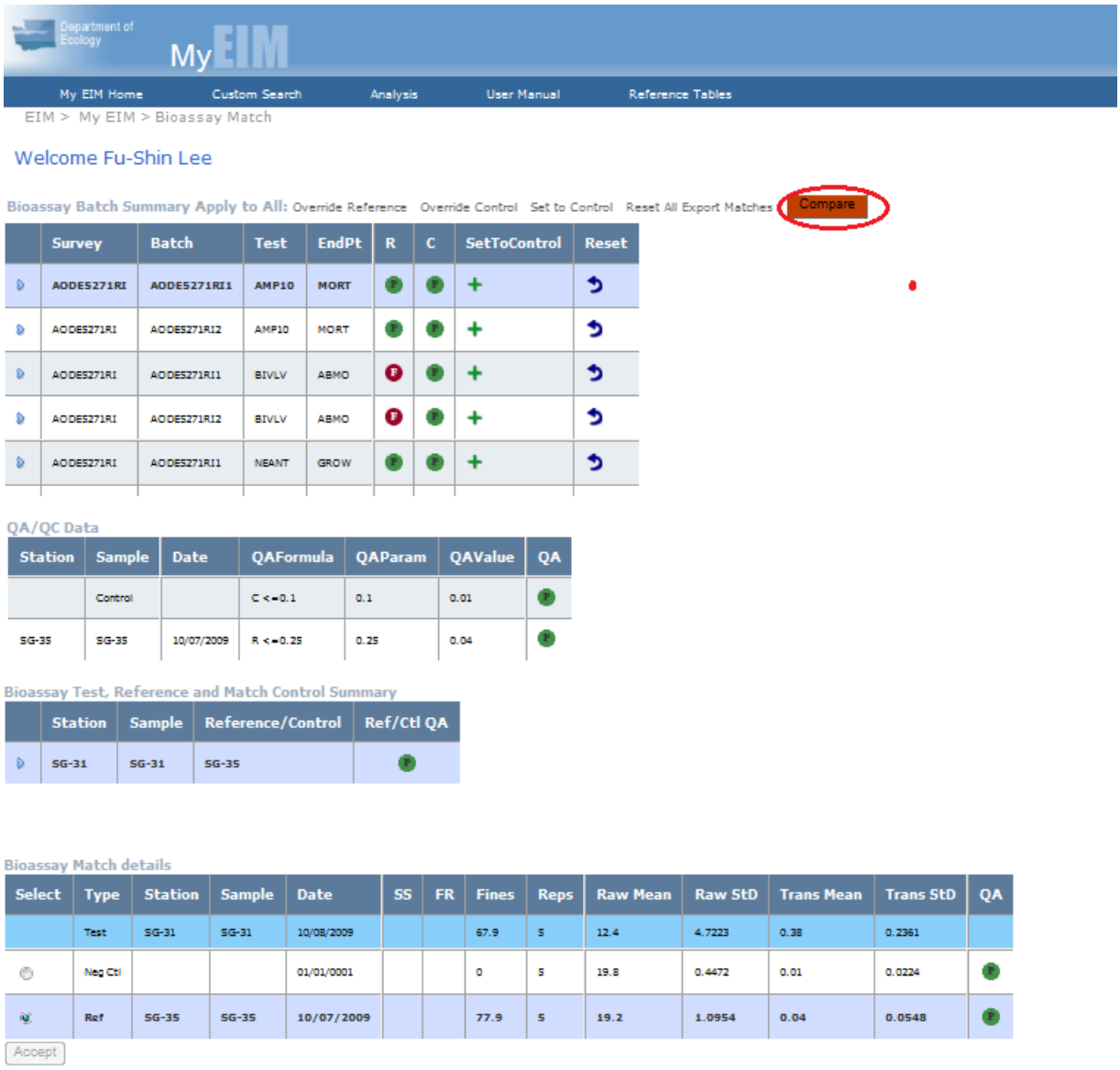


Figure 4 – Bioassay Match Page of MyEIM Bioassay Analysis

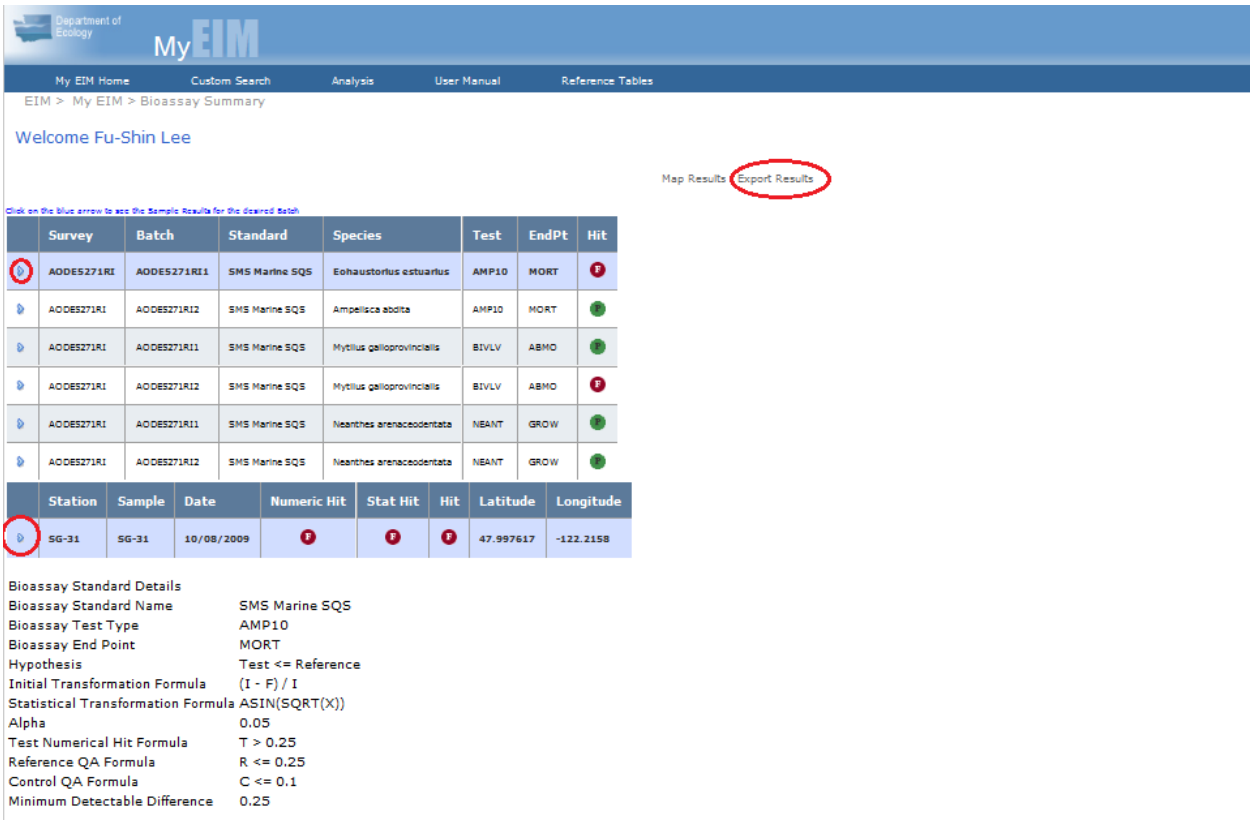


Figure 5 – Bioassay Summary Page of MyEIM Bioassay Analysis

Show All Standards

This checkbox is unchecked by default. When unchecked, the Test Code and Endpoint Code of the results you acquired in the Custom Search application are compared to the Test Code and Endpoint Code of standard criteria. Only the matching criteria show in the list. If no Test Code and Endpoint Code match can be made, then all criteria are displayed.

If "Show All Standards" is checked, all criteria will be displayed, including those that did not match the Test Code and Endpoint Code of your results.

Comparing against criteria of unmatched Test Code and Endpoint Code will return no results for the selected criteria. This option is primarily available to enable the creation of User Defined Cleanup Criteria.

Criteria Grid

The Criteria and Variables grid displays Bioassay Test Criteria. This grid will be discussed in more detail later in this chapter.

Selecting a Standard Cleanup Criteria row

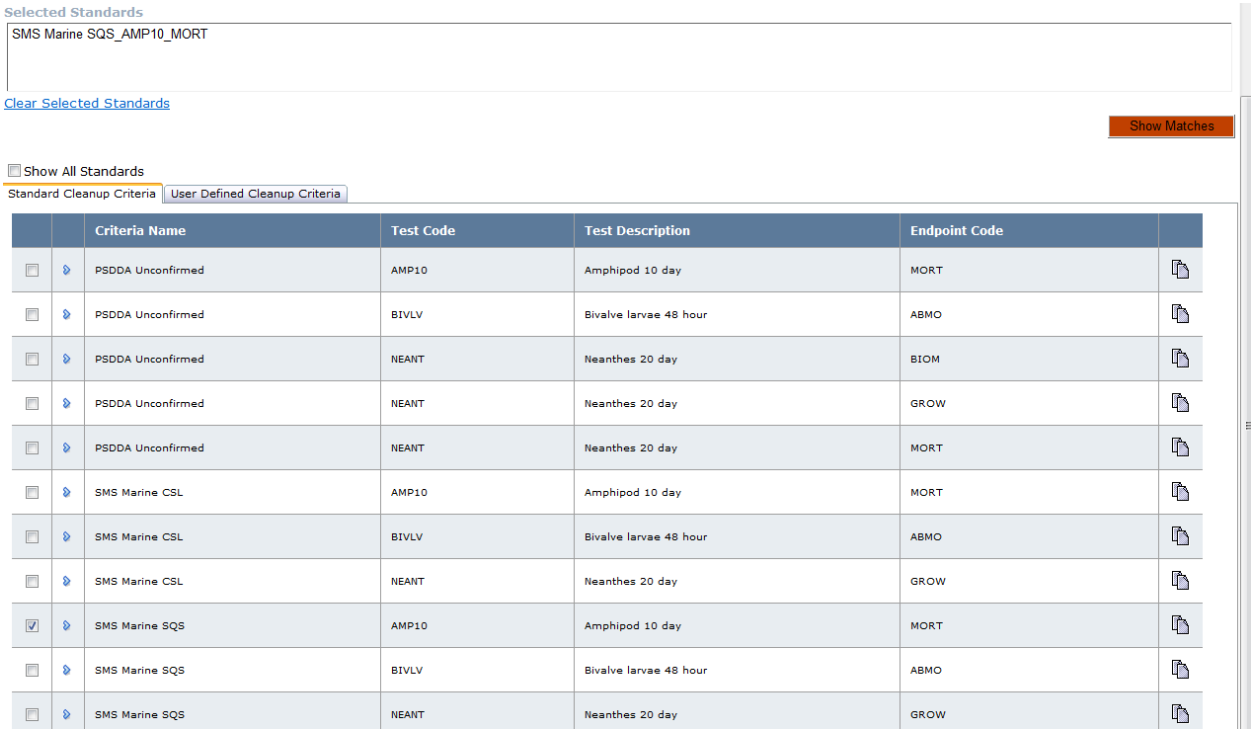


Figure 4 - A standard Cleanup Criteria row.

Clicking on the blue arrow at the beginning of a row will display the details of the selected test as shown in Figure 5.

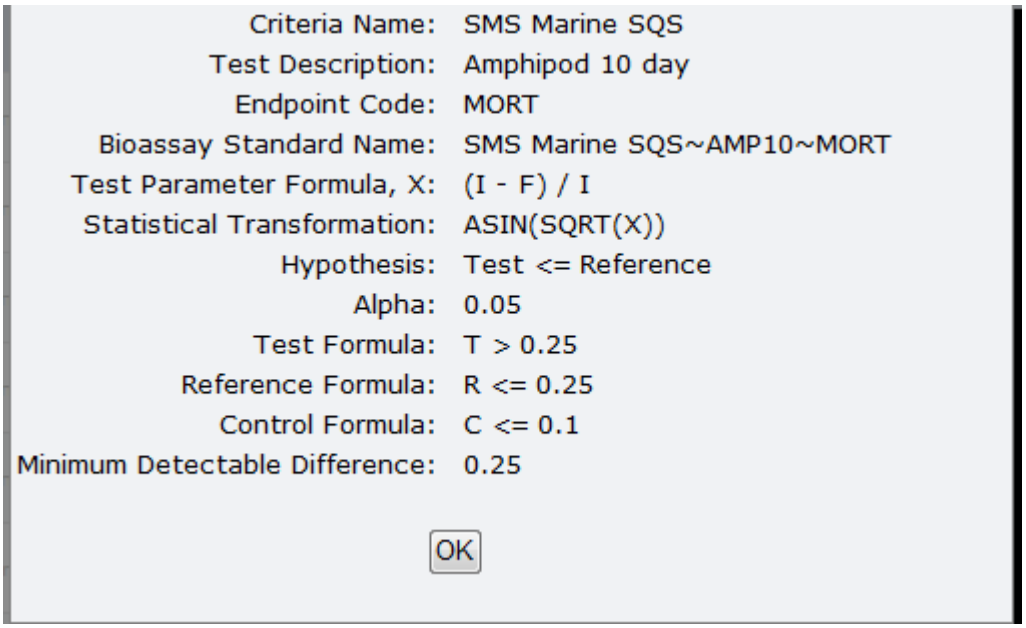
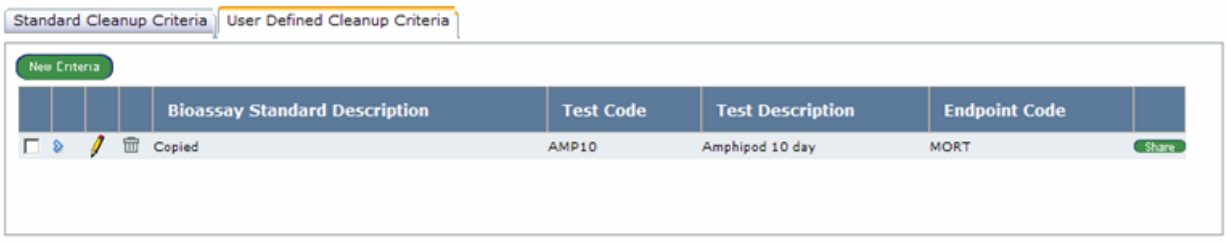


Figure 5 – My EIM Bioassay Analysis - Cleanup Criteria Details

The details include the formula and descriptions of a specific test. Clicking the OK button closes the details popup and returns to the underlying Bioassay Test Parameters page.

Clicking the copy button at the end of the row will create a copy of the Standard under the User Defined Cleanup Criteria tab. This functionality is used for customizing bioassay analysis.

Figure 6 - Copy of a standard Cleanup Criteria



From this new copy, you can make changes to the specification. To view the specification, click the blue arrow at the beginning of the row as shown in Figure 7.

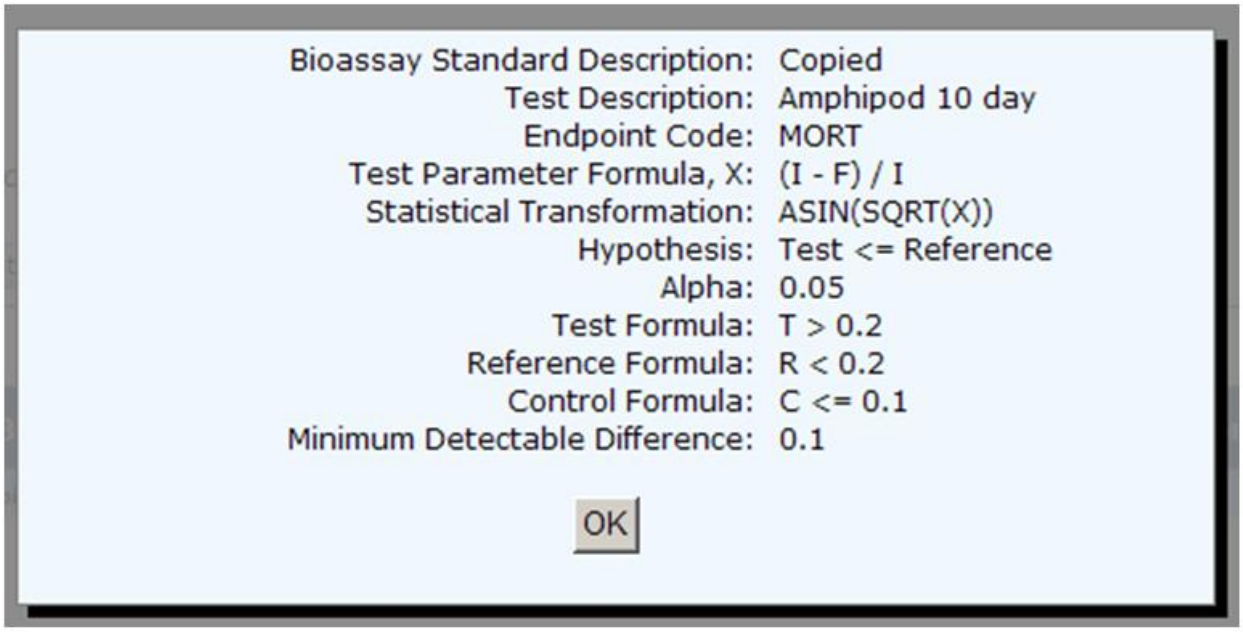


Figure 7 – User Defined Cleanup Criteria Details

Clicking the trash can icon in the same row will delete this Parameter.

To edit the values, you can click the pencil icon as shown in Figure 8.

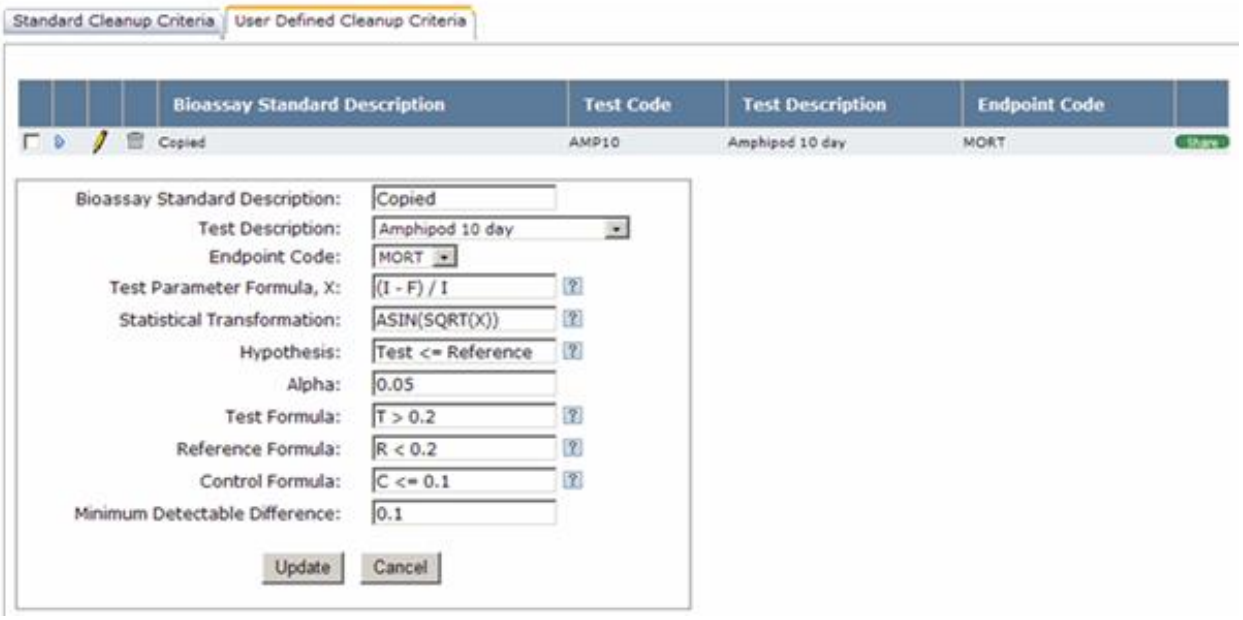


Figure 8 - User Defined Cleanup Criteria in edit mode

Create new values for Bioassay Standard Name, Description, and Initial Transformation. After modifying the values, click Update to save your changes. The question icons next to some selected rows in this window provide guidelines to allowed values in the respective fields. These new transformation formulas can be used in analysis immediately! Clicking the checkbox of the row will select this User Defined standard.

Exercise 1: Comparing Predefined Standards

The simplest analysis that can be performed is to select an existing Standard Cleanup Criteria and choosing Show Matches.

This exercise is using search results from a simple custom bioassay search with User Study ID set to PSDDA_00." Run the search and click "Analyze Data" to get to the Bioassay Test Parameters page.

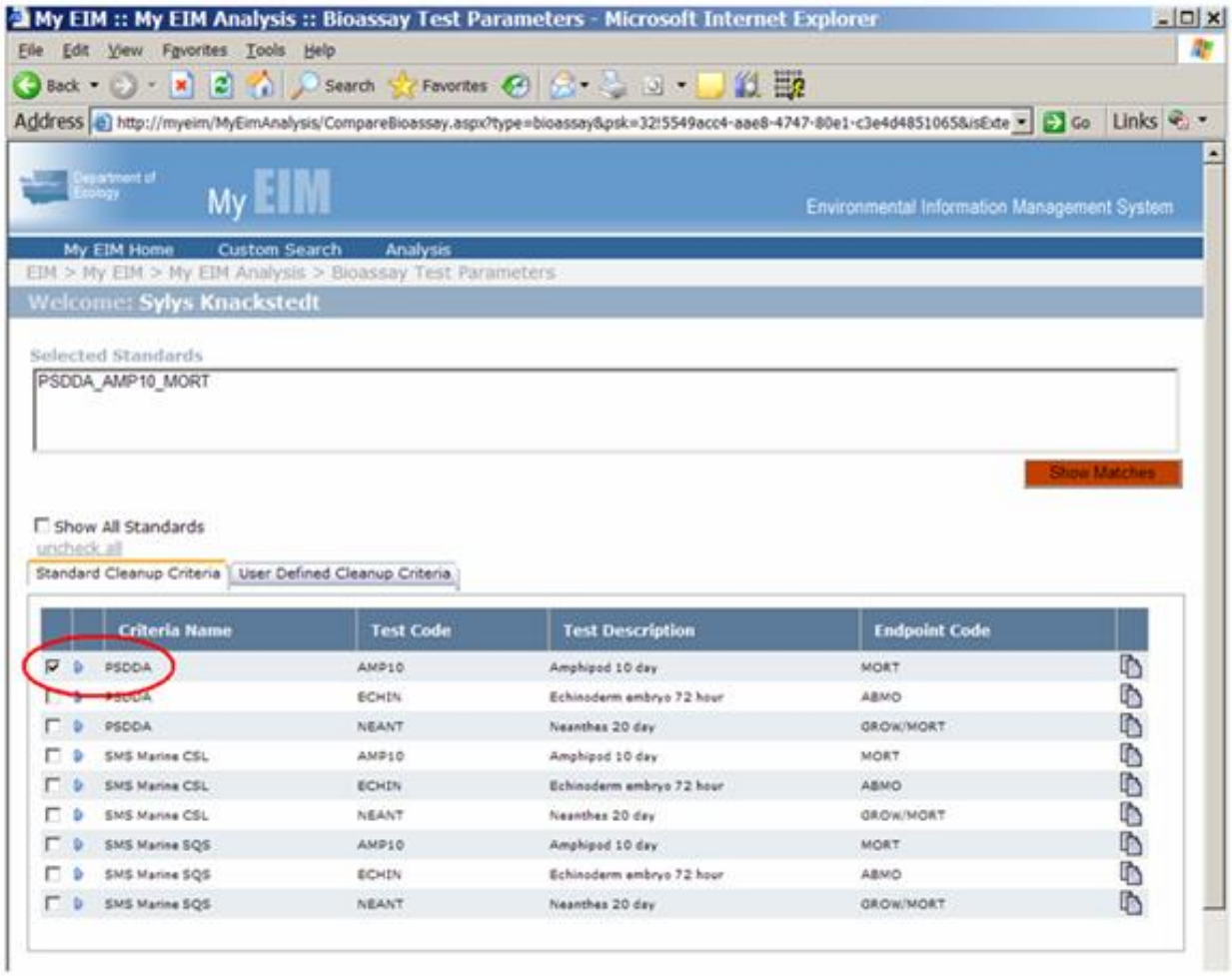


Figure 9 – PSDDA - AMP10 - MORT selected on the Bioassay Test Parameters page.

(1) From the Bioassay Test Parameters page, begin by selecting PSDDA - AMP10 - MORT from the Standard Cleanup Criteria tab.

Note: Once you select an item from the list, it will be added into the Selected Standards list box and the Show Matches button becomes enabled.

(2) Click the Show Matches button. You will be transferred to the Bioassay Match page to choose controls and references.

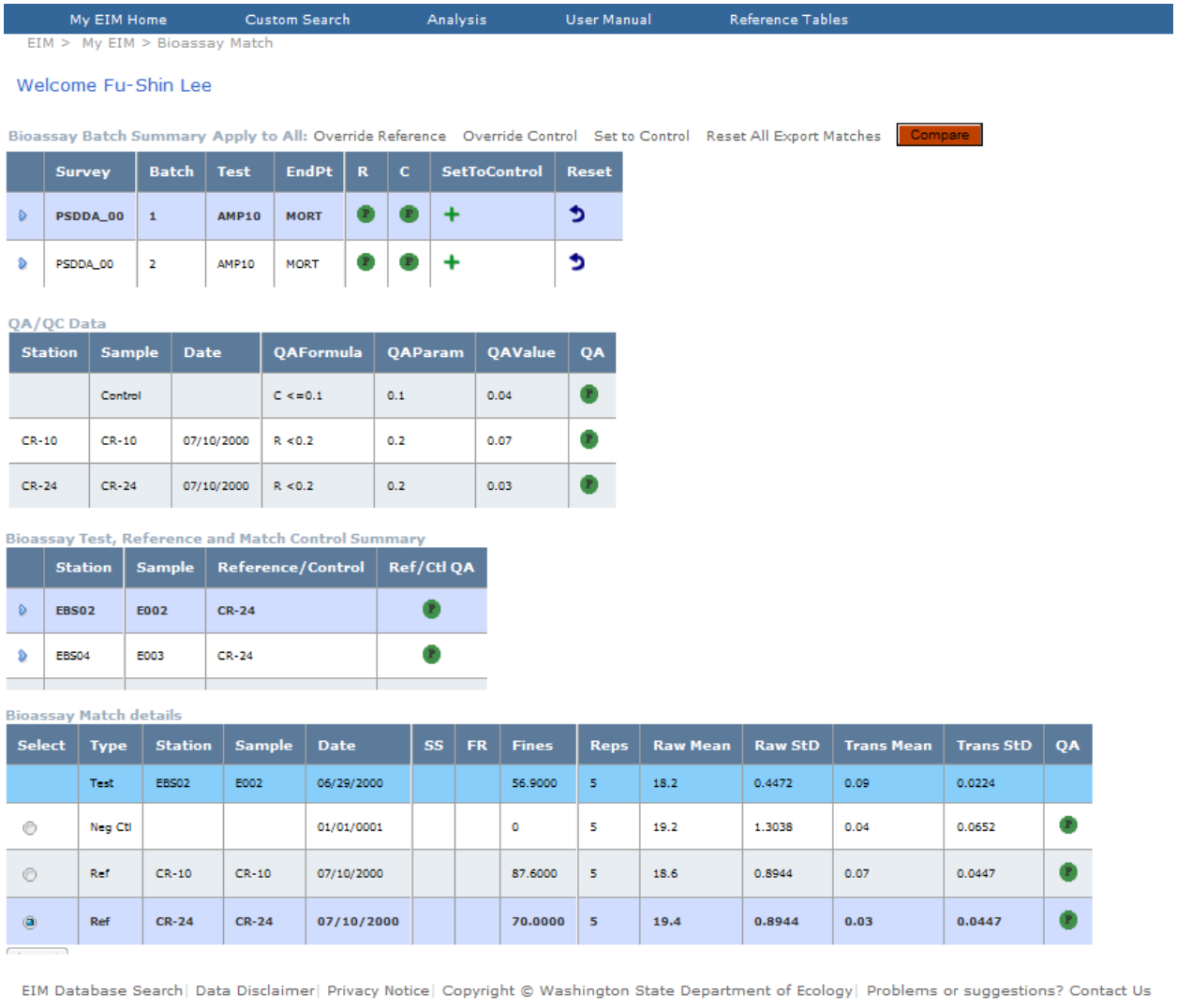


Figure 10 - Bioassay Match Screen

When this page loads, by default the Bioassay Processor will have automatically assigned the controls and references to use for comparison. Details of this process are presented later.

(3) Clicking on ‘Compare’ button will bring you to the Bioassay Summary page to display the bioassay analyzed results.

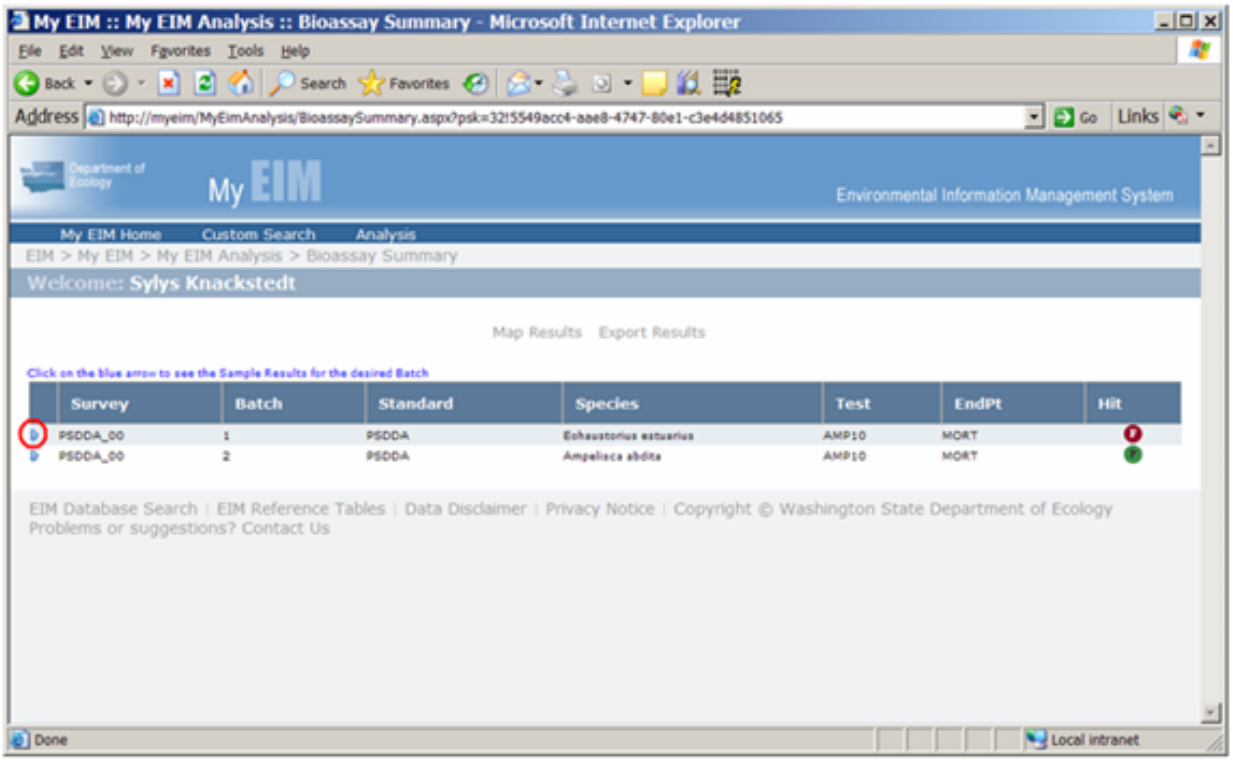


Figure 11 - Bioassay batch comparison results: Selecting batch details.

The results of the Bioassay Analysis are laid out in a single item selectable grid. Click the blue arrows to review the details of this comparison for each batch and again for each sample as shown in Figures 12 and 13.

Clicking on Export Results will show an export dialog box containing a zip file. The zip file will contain a CSV file having complete details of the matches and results, and an html page containing the statistical analysis of each match.

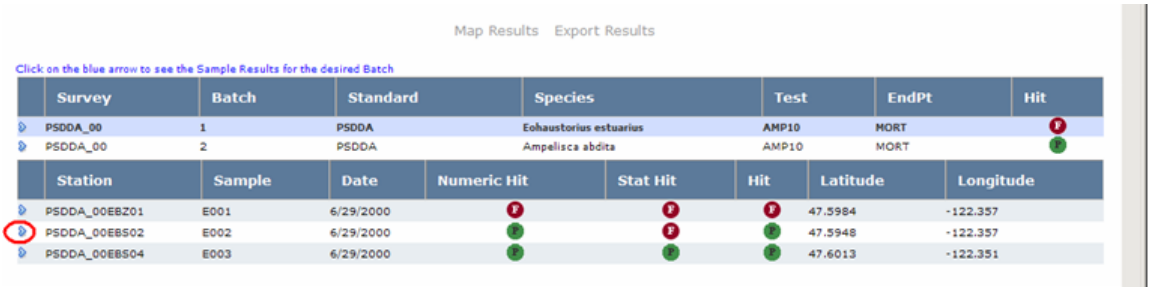


Figure 12 - Bioassay sample comparison results: Selecting sample details.

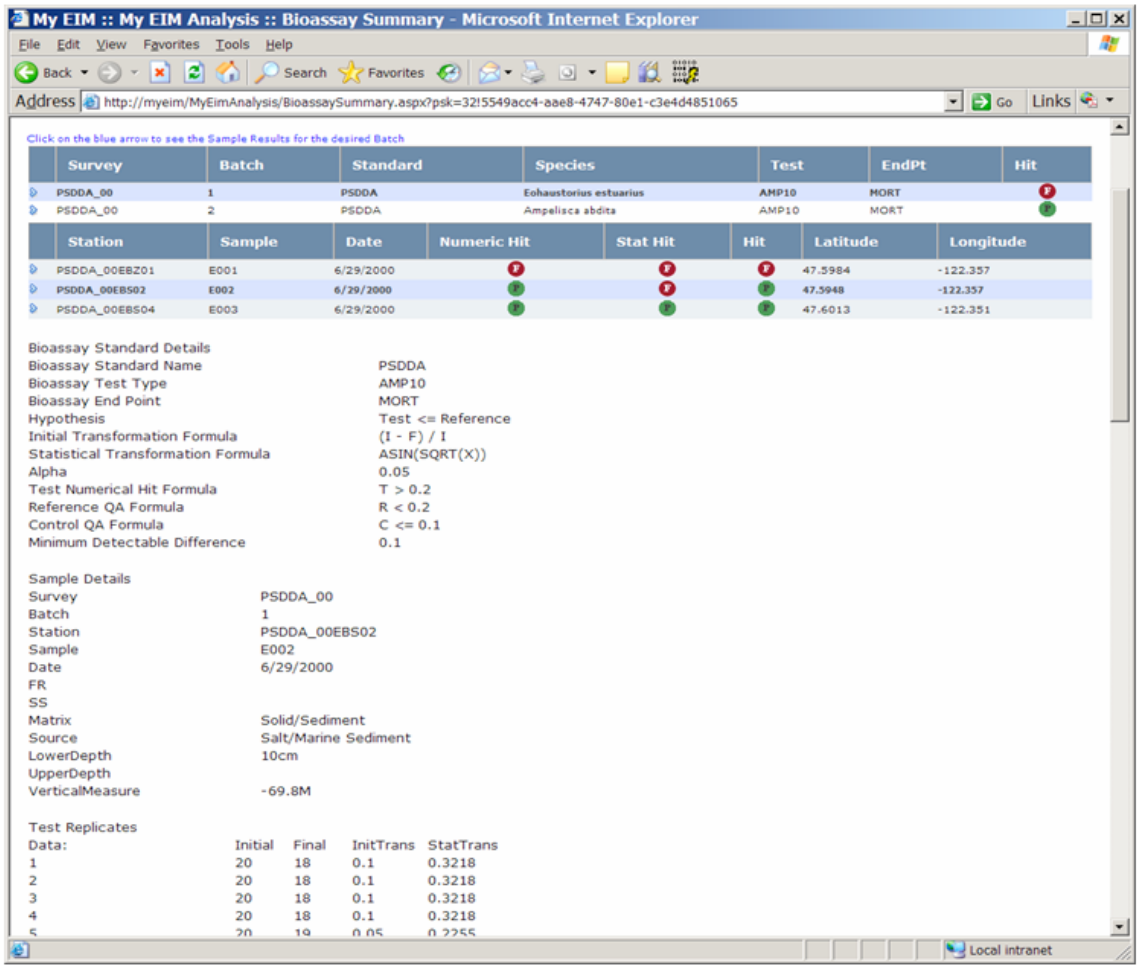


Figure 13 - Bioassay sample comparison details and statistics.

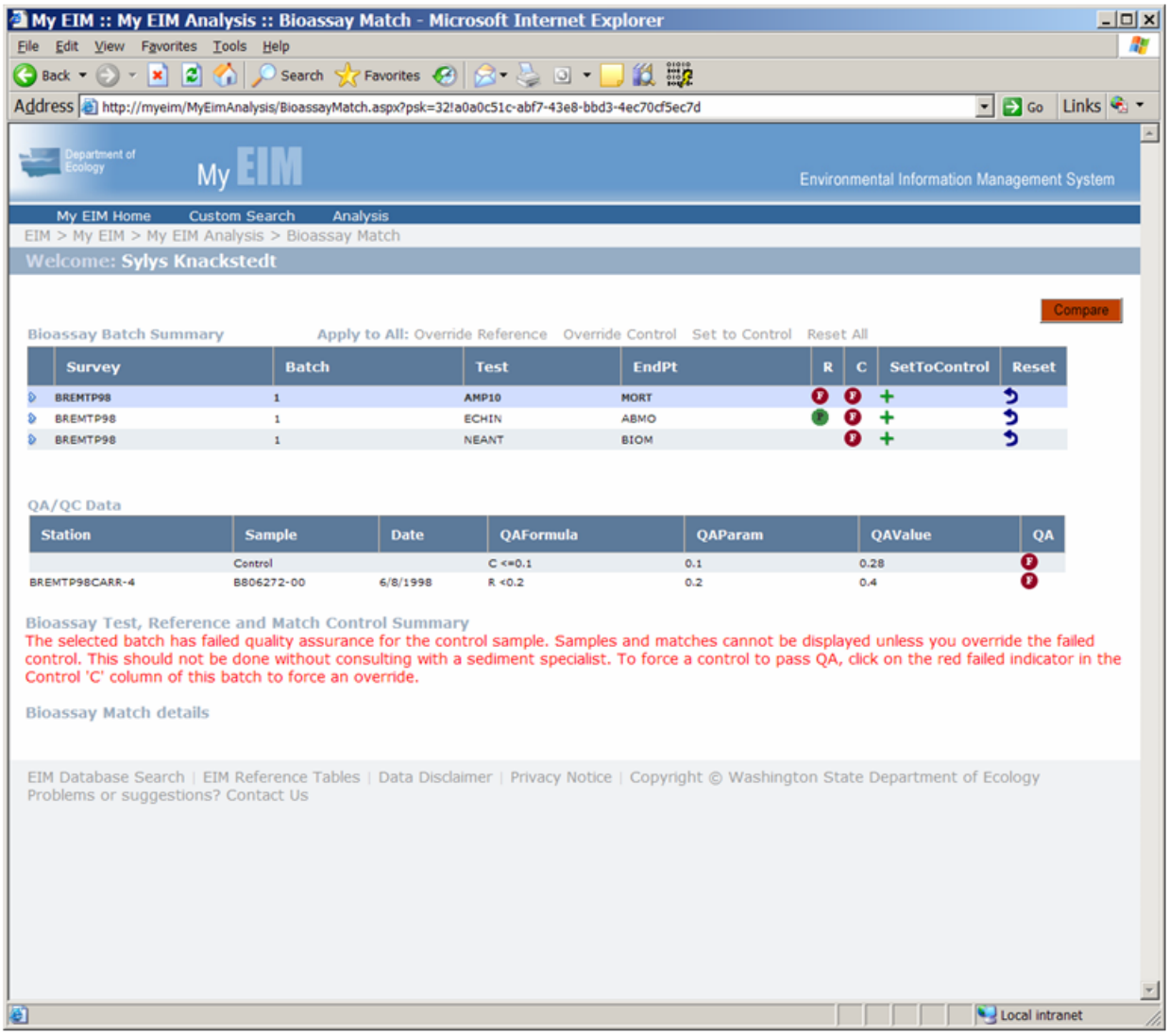
That's it! With just a few clicks you have taken a simple bioassay result set and analyzed it using standard cleanup criteria.

Bioassay Match Page

The Bioassay Match page enables you to select the Controls and References to be used during analysis.

Note: This example uses the Bioassay results data from User Study ID 'BREMTP98'.

Figure 14 – Bioassay Match



The Bioassay match page contains four grids of data. The top grid, Bioassay Batch Summary grid, lists the individual batches of the sample data. Click a blue arrow to select a batch.

For the batch that is selected, the QA/QC Data grid lists its control and reference samples. The control sample is presented in the first row followed by the reference sample in the second row. The formula used to determine QA pass or failure is displayed, along with the QA results.

The third and fourth data grids, the Bioassay Test, Reference and Match Control Summary and the Bioassay Match Details, will only display data for selected batches with control samples that have passed QA.

If the control has failed QA, the following message will appear:

The selected batch has failed quality assurance for the control sample. Samples and matches cannot be displayed unless you override the failed control. This should not be done without consulting with a sediment specialist. To force a control to pass QA, click on the red failed indicator in the Control 'C' column of this batch to force an override.

The message informs you that QA control and reference failures can be overridden in the Bioassay Batch Summary grid, as long as you know what you are doing.

Bioassay Batch Summary Grid and Overriding QA

Note: Don't panic at the complexity of this page! In many cases, you will not need to override the QA and will be able to progress quickly through the Bioassay Match page by simply clicking the orange 'Compare" button.

Each batch has control data which applies to all of the samples in the batch. Quality Assurance (QA) tests are performed against the Reference and Control data. Notice the columns labeled "R" and "C" that stand respectively for Reference and Control.

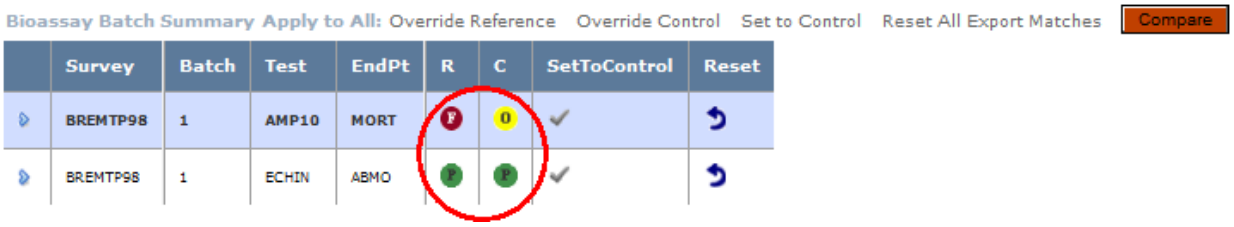


Figure 15 - Reference and control QA

If QA on a batch passes, a green “P” indicator appears in these columns, If QA fails a red “F” button appears. If ANY reference sample within the batch fails QA, a red “F” button will be presented.

Overrides can occur for a single batch or all batches. To override failed QA and force analysis for a single batch, click the red indicator. The indicator will turn into a yellow “O” as a visual indicator that the setting has been overridden.

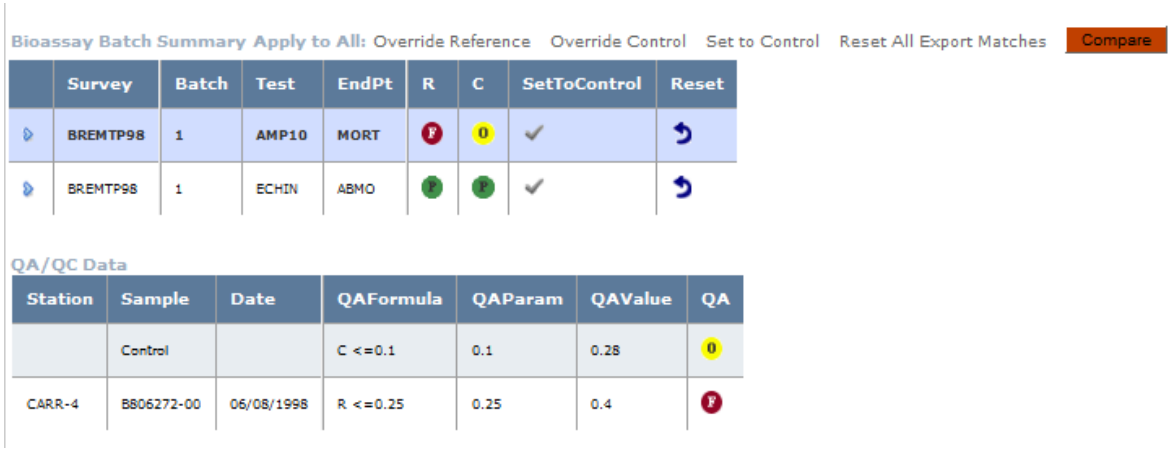


Figure 16 - Control QA has been overridden.

Note: If the selected batch has no Reference samples that batch may not be analyzed by default. In order to analyze that batch user will need to set that batch to match to Control sample if exists.

If a batch has some reference samples with failed QA, it will show as a red “F” button at the batch level. But in the QA/QC data table of this batch there may be some references that are green because they pass QA. If a user overrides the reference QA for that batch, the red “F” button in Bioassay Batch Summary table will turn yellow to indicate that action. The corresponding QA for "reference samples" in QA/QC data table will also turn yellow.

Note: Overriding QA will apply only to those reference samples and control sample that fail QA. If the default QA is a pass, it will always show green.

To revert back to the original default values for a given batch, select the Reset link .

On top of the Bioassay Batch Summary grid are four options that can be applied globally for all data.

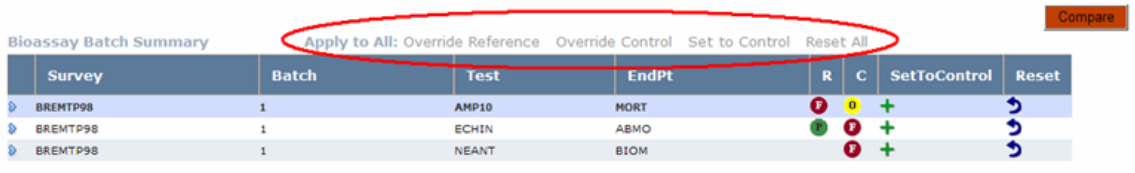


Figure 17 - "Apply to All" controls

Default:

If the batch has no negative control or failed negative control QA, the batch will not be analyzed. If a batch has no reference samples or failed QA for all the reference samples and passed QA for negative control, set the negative control sample to be the reference for each test sample. If a batch does have reference samples, set the reference sample that passes QA and most closely matches the test sample's percent fines to be the reference. The reference sample must pass QA (or have QA overridden for the batch) to be considered for matching.

Override Reference

Clicking this link will override all reference samples that have failed QA for the batches that have passed negative control QA. Re-assign references to all of the test samples in the batch (because the now-overridden reference sample might have a grain size that matches better). This is the equivalent of clicking on all of the red 'F' icons in the 'R' column.

Override Control

Clicking this link will override ALL of the failed negative controls in ALL of the batches to pass QA so that failed negative control QA results are ignored and test samples can be compared to QA passed reference samples, or compared to overridden failed negative control samples when reference QA failed. This is the equivalent of clicking on all the red 'F' icons in the 'C' column.

Set to Control

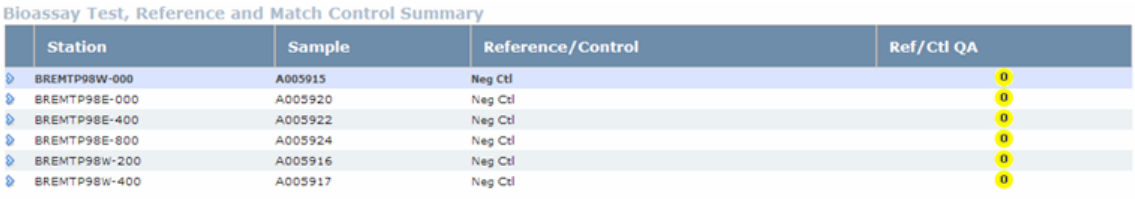
Clicking this link will override all control samples that have failed QA and match ALL test samples to the control samples instead of reference samples for analysis. This is the equivalent of clicking all of the green '+' icons in the 'SetToControl' column.

Reset All

Clicking this link will restore all values back to what was originally displayed when the page was first loaded.

Bioassay Test, Reference, and Match Control Summary

The Bioassay Test, Reference and Match Control Summary shows current match selections for each test sample for the survey and batch of highlighted (selected) row of the "Bioassay Batch Summary" table. It shows the matching reference ID or negative control, and QA status for that sample.


Bioassay Test, Reference and Match Control Summary

Station	Sample	Reference/Control	Ref/Ctl QA
BREMTP98W-000	A005915	Neg Ctl	0
BREMTP98E-000	A005920	Neg Ctl	0
BREMTP98E-400	A005922	Neg Ctl	0
BREMTP98E-800	A005924	Neg Ctl	0
BREMTP98W-200	A005916	Neg Ctl	0
BREMTP98W-400	A005917	Neg Ctl	0

Figure 18 - Bioassay Test, reference, and Match Control Summary

When the Bioassay Match page loads, by default the Bioassay Processor will have automatically assigned the controls and references to use for comparison. This is done using the table shown below as a reference.

Match	Passes QA	What should be the automatic choice?
Reference1	Yes	Reference with closer %fines grain size
Reference2	Yes	
Control	Yes	
Reference1	Yes	Reference1
Reference2	No	

Control	Yes	
Reference1	No	Control
Reference2	No	
Control	Yes	
Reference1	Yes	Batch not analyzed because control failed QA
Reference2	Yes	
Control	No	
Reference1	Yes	Batch not analyzed because control failed QA
Reference2	No	
Control	No	

Bioassay Match Details

This table shows the "test sample" corresponding to highlighted (selected) row of Bioassay Test, Reference and Match Control Summary table and all references and the control, their details for the survey and batch of the highlighted (selected) row of the "Bioassay Batch Summary" table.

The correct matching selection is shown as selected radio button in the "Select" column. You can change the match by selecting a different radio button. The "Accept" button will be enabled when you select a different match, and disabled upon applying the new selection.

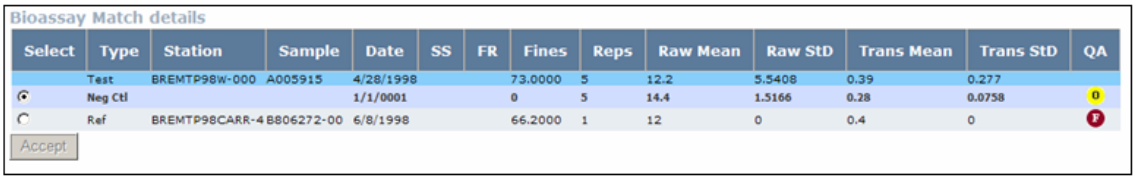


Figure 19 - Bioassay match detail

Clicking the compare button at the upper right will take you to the Display Results (Bioassay Summary) page. From here you can map and export the analyzed results.

Selecting a row in the results grid will open the report of the analysis that has been completed.

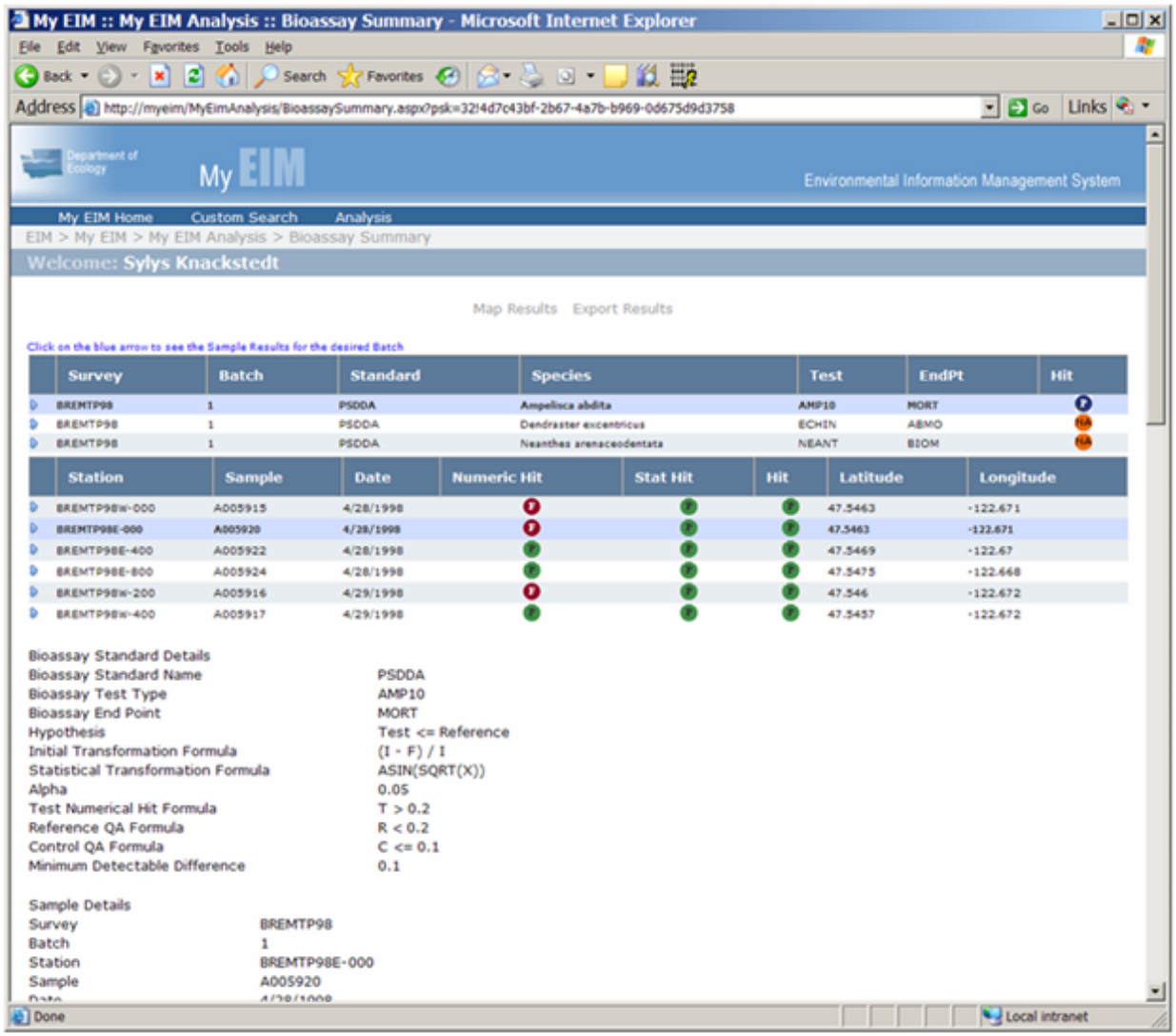


Figure -20 Display results page with detailed report

Clicking Map results link on this page will display the Map with locations where test samples were collected. The locations will show red dots to indicate failed bioassay cleanup criteria.

Export results will show an export dialog box containing a zip file. The zip file will contain a CSV file having complete details of the matches and results, and an html page containing the statistical analysis of each match.

Chapter 7: Tissue Chemistry Analysis

The MyEIM Analysis application provides the tools to perform criteria comparison and statistical analysis of tissue chemistry results queried through the quick start search in Search Templates or your saved search in My Custom Searches or chemistry search in Custom Search.

OVERVIEW OF TISSUE CHEMISTRY ANALYSIS

The MyEIM Analysis application provides tools to compare the searched results of interest to selected cleanup standards (also known as cleanup criteria). The non-regulatory EPA regional 3 fish tissue risked based concentrations for protection of recreational fishers through fish consumption pathway are available under 'Cleanup Criteria' tab in MyEIM. Users are not restricted to compare searched results to predefined cleanup standards. MyEIM Analysis provides an interface for you to define your own set of standards and derived variables using user defined cleanup criteria and user defined derived variables.

This chapter consists of three sections, Tissue Chemistry Data Search, Standard Analysis and Customizing My Analysis. Tissue Chemistry Data Search will show you the steps necessary to perform in preparation for data analysis. Standard Analysis will cover the use of predefined cleanup criteria as the basis of analysis. Customizing My Analysis will discuss various user definable aspects of the application. Several exercises will help demonstrate the use of the various features.

Note: Before we begin, this chapter assumes that you have already learned how to acquire data result set using the Search application and prepare for analysis. If you need to review how to search the EIM data of your interest to work with, please refer to the Home and Search chapters.

TISSUE CHEMISTRY DATA SEARCH

To begin the analysis process, you will first have to get a result set from the quick start search template (Chemistry tissue data check) in Search Templates or your saved search in My Custom Search or chemistry search in Custom Search.

Note: If you need a tissue chemistry result set to get started, select 'Chemistry tissue data check' in Search Templates of the 'Home' page. Clicking on 'Save As' will bring you to the 'Chemistry Search' page. Clicking on 'Show Data' will bring you to the Results page for the searched Chemistry Data.

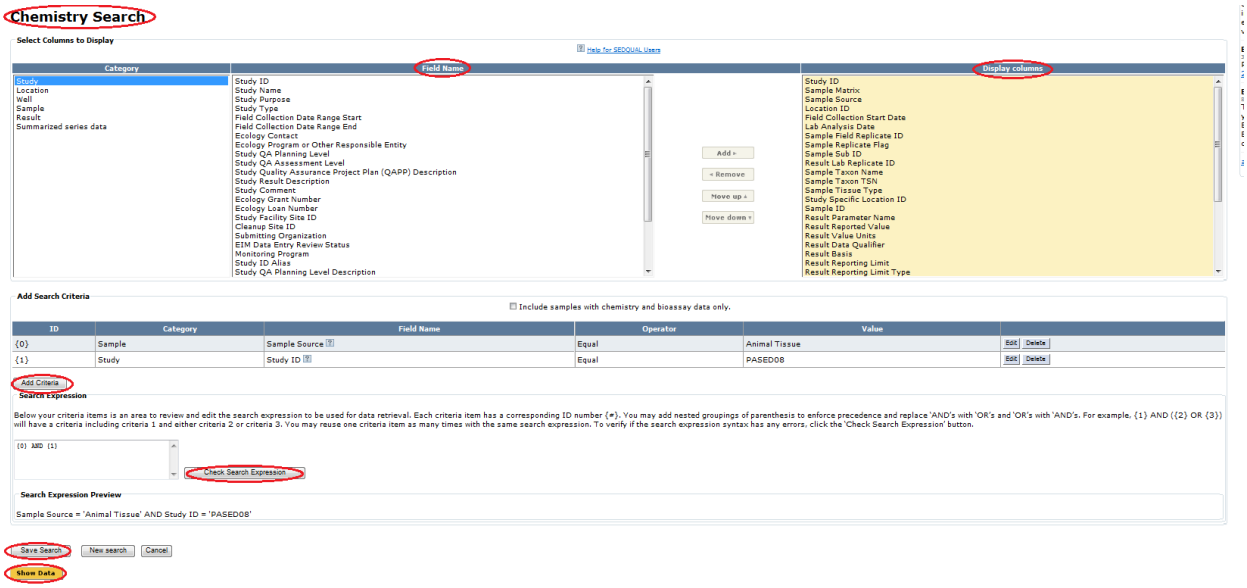
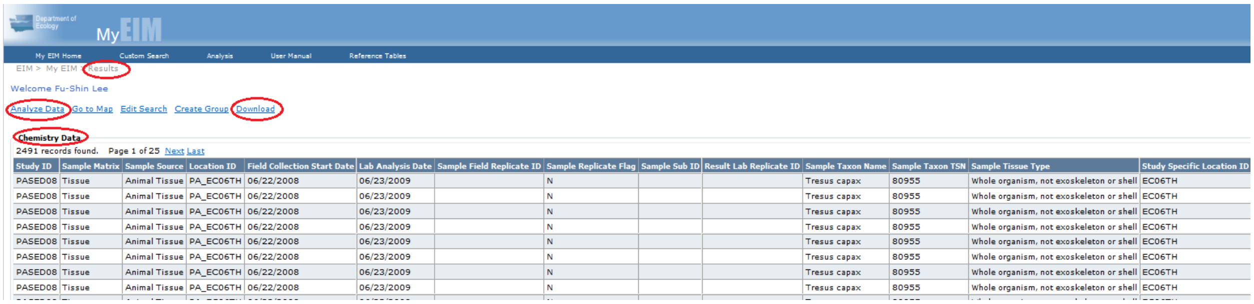


Figure 2 - MyEIM Chemistry Search Page for Tissue Chemistry Data

On the searched Results page for Chemistry Data, click the 'Analyze Data' link in the upper left corner of the content page. This link will take you to the "Choose Comparison Criteria" page of the Analysis application.



Study ID	Sample Matrix	Sample Source	Location ID	Field Collection Start Date	Lab Analysis Date	Sample Field Replicate ID	Sample Replicate Flag	Sample Sub ID	Result Lab Replicate ID	Sample Taxon Name	Sample Taxon TSN	Sample Tissue Type	Study Specific Location ID
PASED08	Tissue	Animal Tissue	PA_EC06TH	06/22/2008	06/23/2009		N			Tresus capax	80955	Whole organism, not exoskeleton or shell	EC06TH
PASED08	Tissue	Animal Tissue	PA_EC06TH	06/22/2008	06/23/2009		N			Tresus capax	80955	Whole organism, not exoskeleton or shell	EC06TH
PASED08	Tissue	Animal Tissue	PA_EC06TH	06/22/2008	06/23/2009		N			Tresus capax	80955	Whole organism, not exoskeleton or shell	EC06TH
PASED08	Tissue	Animal Tissue	PA_EC06TH	06/22/2008	06/23/2009		N			Tresus capax	80955	Whole organism, not exoskeleton or shell	EC06TH
PASED08	Tissue	Animal Tissue	PA_EC06TH	06/22/2008	06/23/2009		N			Tresus capax	80955	Whole organism, not exoskeleton or shell	EC06TH
PASED08	Tissue	Animal Tissue	PA_EC06TH	06/22/2008	06/23/2009		N			Tresus capax	80955	Whole organism, not exoskeleton or shell	EC06TH
PASED08	Tissue	Animal Tissue	PA_EC06TH	06/22/2008	06/23/2009		N			Tresus capax	80955	Whole organism, not exoskeleton or shell	EC06TH
PASED08	Tissue	Animal Tissue	PA_EC06TH	06/22/2008	06/23/2009		N			Tresus capax	80955	Whole organism, not exoskeleton or shell	EC06TH

Figure 2 - MyEIM Results Page

Custom Search automatically hands off the results at the back end to Analysis when you come into the Analysis application.

STANDARD ANALYSIS

Two following pages for chemistry data analysis will be shown in the order of analysis process:

- Choose Comparison Criteria
- Analysis Results

CHOOSE COMPARISON CRITERIA PAGE

The first step in the Analysis process is to collect settings for the analysis on the data received from the Chemistry Search application. The *'Choose Comparison Criteria'* page is the first step in analyzing your data. It is important to note the different elements of this page which consist of the following components:

At the top of the page is the Welcome banner displaying user's name and MyEIM navigation menu. Below this banner is the data Analysis Type (e.g., Sediment Chemistry, MTCA, Tissue Chemistry) and Selected Standards list box which displays the standards you have selected to compare your searched chemistry data against. To the right of the Analysis and Selected Standards is the 'Selected Preferences' summary. A prominent 'Compare' button is just below the Selected Preferences summary detail container. The Show All Standards checkbox sits below the 'Clear Selected Standards' link. The Criteria and Variables grid is the main grid on the page, organized by a set of page tabs, Cleanup Criteria, User Defined Cleanup Criteria, Derived

Variables and User Defined Derived Variables, which allows the users to select established and/or user defined cleanup criteria, and to create user defined cleanup criteria and derived variables. Clicking on the blue arrow next to the selected standard or variable will show you the constituents of the selected criteria and variable at the bottom of the page in Figure 3a.

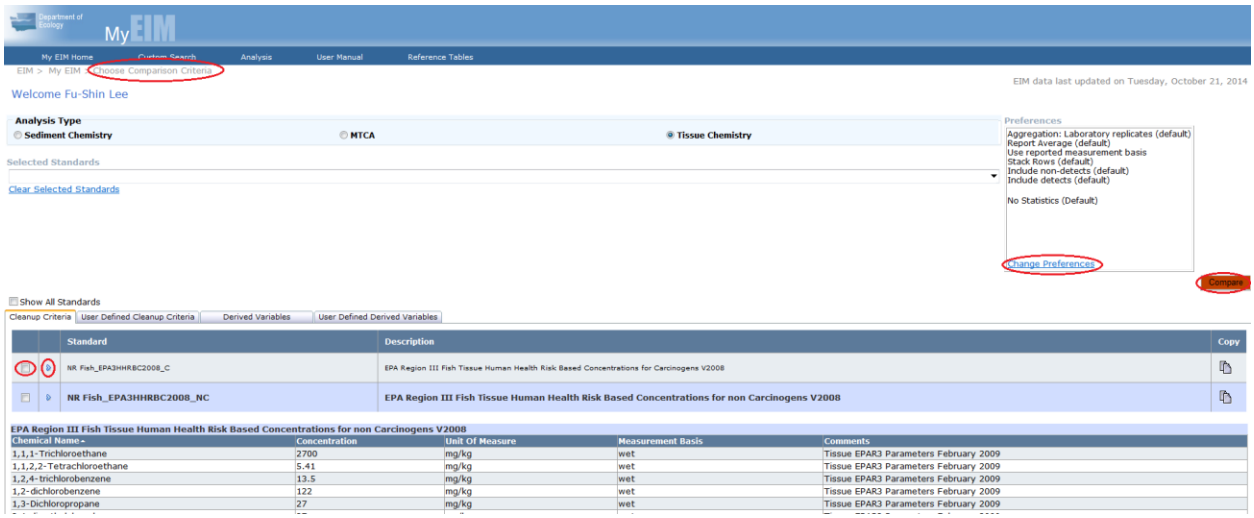


Figure 3a - MyEIM Analysis - Choose Comparison Criteria Page

The options and features in the 'Choose Comparison Criteria' page are detailed below.

Analysis Type

MyEIM supports analyses of Sediment data, MTCA data (soil and water), and Tissue data. These three types of analyses differ in the data reduction logic and statistical options. MyEIM will identify the most matching analysis type based on the sample source of data you search. Tissue Chemistry was selected in this screen shot, since Animal Tissue was selected for Sample Source in MyEIM Chemistry Search page. Users need to decide what type of analysis is appropriate for the data obtained from custom query. MyEIM is currently designed to analyze one sample source of searched data each time.

CLEANUP CRITERIA

Cleanup Criteria is one of four options under the Cleanup Criteria and Derived Variables grid. MyEIM Cleanup criteria have the non-regulatory EPA region 3 tissue risk based concentrations for human health protection via recreational fish consumption pathway. MyEIM will display the applicable cleanup criteria per selected specific sample source of searched chemistry data. For example, when animal tissue is selected as the sample source of the searched chemistry fish tissue data, cleanup criteria will automatically display the non-regulatory EPA region 3 tissue risk based concentrations for human health protection via recreational fish consumption pathway. The criteria housed under Cleanup Criteria will be updated, when the regulatory or non-regulatory criteria are updated.

Selected Standards

This box will display the list of standards (also called "comparison criteria") that have been selected for analysis. Criteria are added or removed from this box by checking or un-checking the rows in the Cleanup Criteria and User Defined Cleanup Criteria grids.

Selected Preferences

The Selected Preferences summary box displays the analysis options that will be used during the execution of the analysis. You have access to the Analysis Criteria settings by clicking the 'Change Preferences' link at the bottom left corner of the Selected Preferences summary. If you review the preferences, in order to return to the criteria selection page, click 'OK' to accept your changes or 'Cancel' button to accept existing settings.

The Preferences pop up window has two major groups of options, Analysis Criteria and Statistical Parameters. The Analysis Criteria provide the options on how and what data will be treated, aggregated and reported based on the selected options. The Statistics Parameters provide the options on how the data will be statistically analyzed and reported per the analyzed results based on the selected analysis criteria. Statistical analysis and display depend on all analysis and statistical settings selected in Preferences.

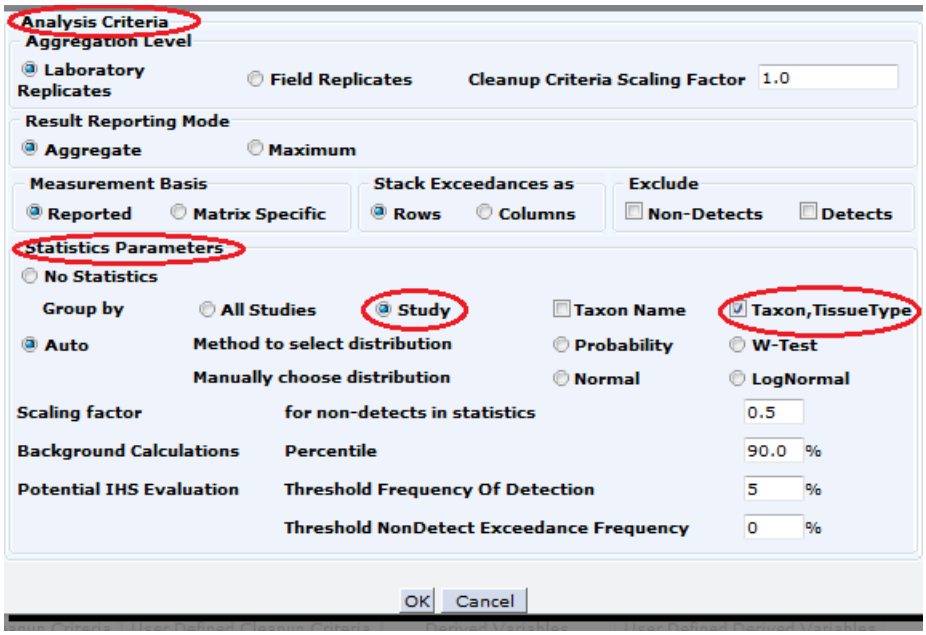


Figure 3b: Change Preferences Dialog for Tissue Chemistry

The option groups in 'Analysis Criteria' have settings for how the data will be aggregated for criteria comparison and derived variable calculations, how the data will be compared to the adjusted cleanup criteria using Cleanup Criteria Scaling Factor, as well as output results display options. The options for Analysis Criteria will be detailed under ANALYSIS CRITERIA.

The 'Statistics Parameters' group has settings used exclusively for statistical analysis. The 'Statistics Parameters' group has settings used exclusively for tissue data statistical analysis (Taxon Name and Tissue Type). However statistical analysis and display depend on all analysis and statistical settings.

ANALYSIS CRITERIA

Aggregation Level

MyEIM allows you to perform data reduction at Laboratory Replicates level to give one value corresponding for multiple laboratory replicate results, or, at Field Replicates level to give one value for multiple field replicate results. Laboratory Replicates aggregation level is chosen by default for Tissue Chemistry Analysis Type.

Result Reporting Mode

This sets the rule for data reduction. MyEIM provides two options: Aggregate rule and maximum rule. Please refer to Appendix E for details on how these rules are implemented.

Measurement Basis

By default, reported measurement basis is used for all calculations. In cases where measurement basis is not reported or wrongly reported, MyEIM allows users to override the reported measurement basis with a matrix specific measurement basis (assign 'wet' for all tissue chemistry data). In order to assign an override value automatically where appropriate, you will need to select 'Matrix Specific' option.

Stack Exceedances As

"Stacking Exceedances" refers to the output of the multiple criteria comparison analysis results. Take as an example a comparison with two criteria.

If Stack Exceedances is set to "Columns," then for each row in the data results, there will be one row in the analyzed results. Each of these rows will have full sets of analysis columns, one for each chosen criteria. This option is currently not working, and will be addressed when the end users see the strong needs of using it.

ChemicalName	0_CriteriaName	0_ChemicalConc	0_CriteriaConc	0_CriteriaUOM	0_CriteriaBasis	0_Exceedance	0_HitOrNot	0_Comment	1_CriteriaName	1_ChemicalConc	1_CriteriaConc
dichlorobenzidine;3,3'-									NR Fish_EPA3HHRBC2008_C	0.023	0.007
aluminum	NR Fish_EPA3HHRBC2008_NC	16	1400	mg/kg	wet	0.01215		OK			
antimony	NR Fish_EPA3HHRBC2008_NC	0.05	0.54	mg/kg	wet	0.09242		OK			
arsenic	NR Fish_EPA3HHRBC2008_NC	2.6	0.41	mg/kg	wet	6.502	Hit	OK	NR Fish_EPA3HHRBC2008_C	2.6	0.0021
barium and compounds	NR Fish_EPA3HHRBC2008_NC	0.99	270	mg/kg	wet	0.003674		OK			
beryllium	NR Fish_EPA3HHRBC2008_NC	0.05	2.7	mg/kg	wet	0.01852		OK			
bis(2-ethylhexyl) phthalate	NR Fish_EPA3HHRBC2008_NC	0.1	27	mg/kg	wet	0.003704		OK	NR Fish_EPA3HHRBC2008_C	0.1	0.22
cadmium	NR Fish_EPA3HHRBC2008_NC	0.55	1.4	mg/kg	wet	0.4096		OK			
Cobalt	NR Fish_EPA3HHRBC2008_NC	0.26	0.41	mg/kg	wet	0.6355		OK			

Figure 4a – Analyzed results stacked in columns. Notice the 0_ and 1_ in front of the column names.

If “Rows” is selected, the grid will have multiple analyzed rows for each data result; one for each chosen criteria group.

ChemicalName	CriteriaName	ChemicalConc	CriteriaConc	CriteriaUOM	CriteriaBasis	Exceedance	HitOrNot	Comment
dichlorobenzidine;3,3'-	NR Fish_EPA3HHRBC2008_C	0.023	0.007	mg/kg	wet	3.281	Hit	OK
aluminum	NR Fish_EPA3HHRBC2008_NC	16	1400	mg/kg	wet	0.01215		OK
antimony	NR Fish_EPA3HHRBC2008_NC	0.05	0.54	mg/kg	wet	0.09242		OK
arsenic	NR Fish_EPA3HHRBC2008_NC	2.6	0.41	mg/kg	wet	6.502	Hit	OK
arsenic	NR Fish_EPA3HHRBC2008_C	2.6	0.0021	mg/kg	wet	1257	Hit	OK
barium and compounds	NR Fish_EPA3HHRBC2008_NC	0.99	270	mg/kg	wet	0.003674		OK
beryllium	NR Fish_EPA3HHRBC2008_NC	0.05	2.7	mg/kg	wet	0.01852		OK
bis(2-ethylhexyl)	NR	0.1	27	mg/kg	wet	0.003704		OK

Figure 4b – Analyzed results stacked in rows. Notice Chemical Name is duplicated if in criteria.

Exclude

Check the box next to either Detects or Non-Detects to exclude them from the results output (Selecting both Non-Detects and Detects will forcefully exclude ALL results output).

Statistics Parameters

MyEIM allows users to compute statistics on data aggregated concentrations for every chemical reported in each study or across several studies. Tissue data statistics can also be performed based on ‘Taxon name’ or ‘Taxon Name and Tissue Type’. Please refer to the chapter 9 on ‘Statistical Analysis of MyEIM Tissue Data’ section for details.

Compare Button

Clicking this button will begin the analysis processing. All of the settings you have chosen will be sent to MyEIM processors for analysis.

Clear Selected Standards

Clicking this link will unselect both standard and user defined cleanup criteria listed in selected standards list.

Show All Standards Checkbox

By default, this box remains unchecked. In this case, only the criteria that have the same sample matrix and sample source as your search results will appear under the "Standard Cleanup Criteria" tab.

If the 'Show All Standards' box is checked, all standard criteria will be displayed, including those that can't be matched to your search results based on sample matrix and sample source.

Note: The analysis processor will compare search results to any standards even if they are incompatible in terms of sample matrix and sample source. This feature is made available for cross media analysis, however, caution is advised. In any case, the comparison will be made only if measurement basis and unit of measurement are compatible with those of the chosen criteria.

Criteria and Variables Grid

The Criteria and Variables grids display Standard Criteria, User Defined Criteria, Derived Variables and User Defined Derived Variables, and, constituents in each of these four types of criteria items. These four grids will be discussed in detail as we progress in this chapter.

Constituents List

The Constituents List displays detailed information for the selected standard. The list can be exported to excel for easy download.

Cleanup Criteria tab

The simplest analysis that can be performed is to select an existing Comparison Criteria and then to click "Compare" button. This can be done by selecting criteria from the list under this tab.

User Defined Cleanup Criteria tab

Users can customize criteria and use those criteria for comparison. This feature will be discussed later in this chapter.

Derived Variables tab

This tab lists available standard derived variables. There are two types of standard derived variables, Simple Derived Variables and Weighted Derived Variables. Simple derived variables had all constituents equally weighted. In weighted derived variables, constituent weights are fractions. Simple derived variables include Total Benzofluoranthenes (BFA), Polychlorinated Biphenyls (PCBs), Low Molecular Weight Polycyclic Aromatic Hydrocarbons (LPAH), High Molecular Weight Polycyclic Aromatic Hydrocarbons (HPAH), PCB Aroclor Sum, PCB Congener Sum, Total PAHs, Total DDDs, Total DDEs, and Total DDTs. Weighted derived variables include Carcinogenic Polycyclic Aromatic Hydrocarbons as TEQs (cPAH-TEQ), Dioxin/Furan-TEQ, Dioxin-like PCB TEQ and Total 2,3,7,8-TCDD TEQ. Weighted derived variables need to be defined in the user defined cleanup criteria in order to be calculated, compared to the criteria and displayed in the results output, if they are not defined in the selected cleanup criteria.

User Defined Cleanup Criteria and User Defined Derived Variables tab

Users can customize derived variables and cleanup criteria of their interest in the User Defined Cleanup Criteria and User Defined Derived Variables. This feature will be discussed later in this chapter.

EXERCISE 1: COMPARING TO PREDEFINED CLEANUP CRITERIA

(1) After you click on sitting at left to 'Chemistry tissue data check', clicking on 'Save As' shown in Figure 5a of MyEIM Home page will bring you to the 'Chemistry Search' page in Figure 5b. The 'Chemistry Search' page shows all the display columns with all the selected EIM data fields used for the chemistry tissue data check, analysis, and interpretation for specified study, PASED08.

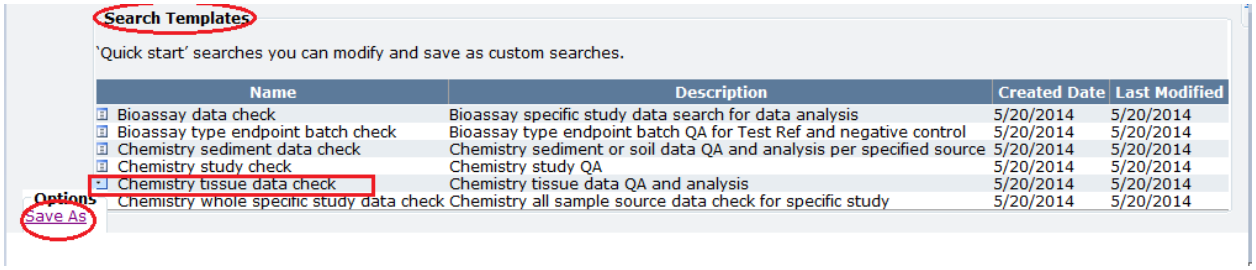


Figure 5a – Search Templates in MyEIM Home Page

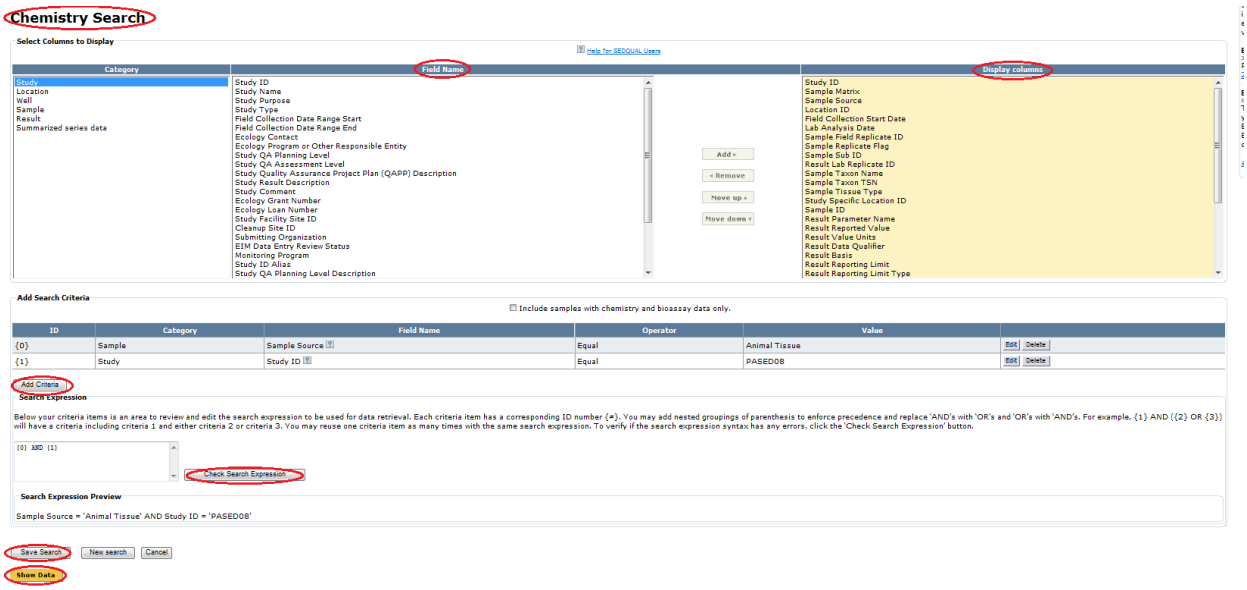


Figure 5b - Chemistry Search Page for Tissue Data Check

Click 'Show Data'.

(2) This will take you to preview of the query results page.

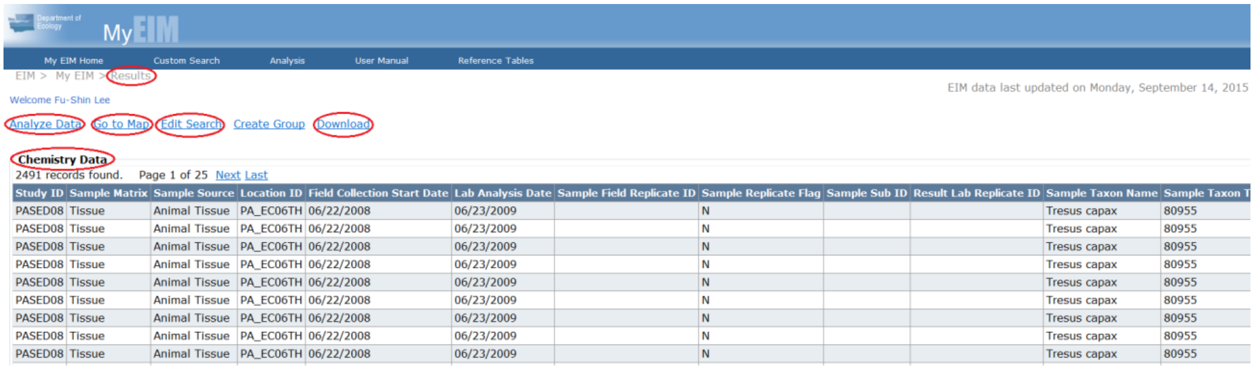


Figure 6 - Results Page for Searched Tissue Data

Click on ‘Analyze data’.

(3) Under the Cleanup Criteria Tab, check on the boxes  left to NR Fish_EPA3HHRBC_C and NR Fish_EPAR3HHRBC_NC in Figure 5-3. These selected standards will be shown in the ‘Selected Standards’ box.

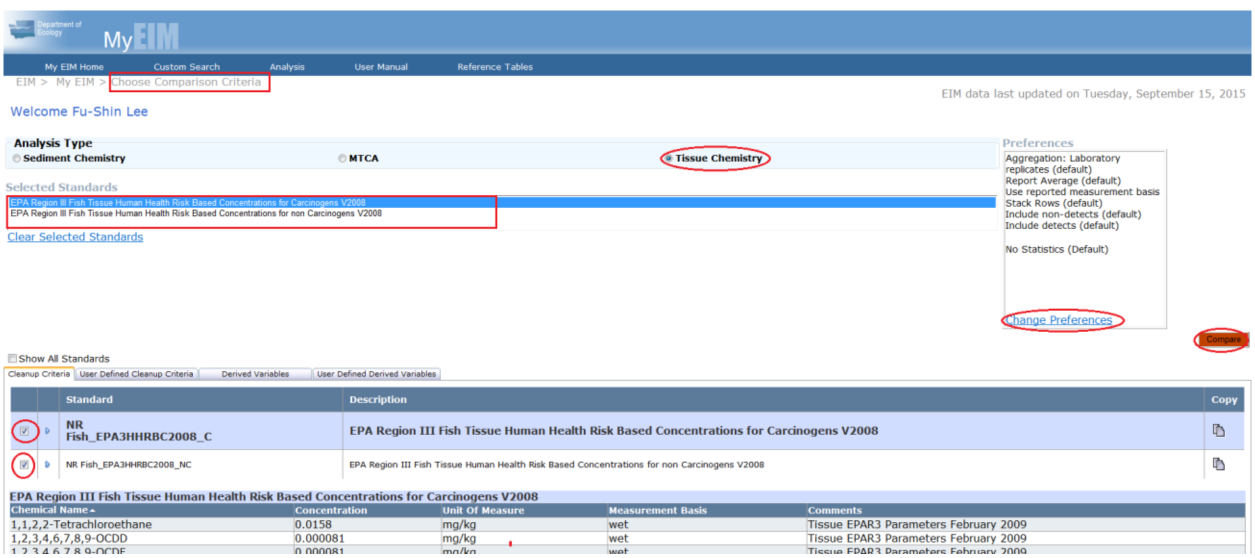


Figure 7 – NR Fish EPA Region 3 HHRBC Selected on Choose Comparison Criteria Page

 Note: Once you select an item from the list, it will be added into the Selected Standards.

(4) Click the Compare button. You will be transferred from Choose Criteria Comparison page to the Processor page while the analysis is being performed.

This page will display the process status, along with the total number of rows received from the database and from analysis.

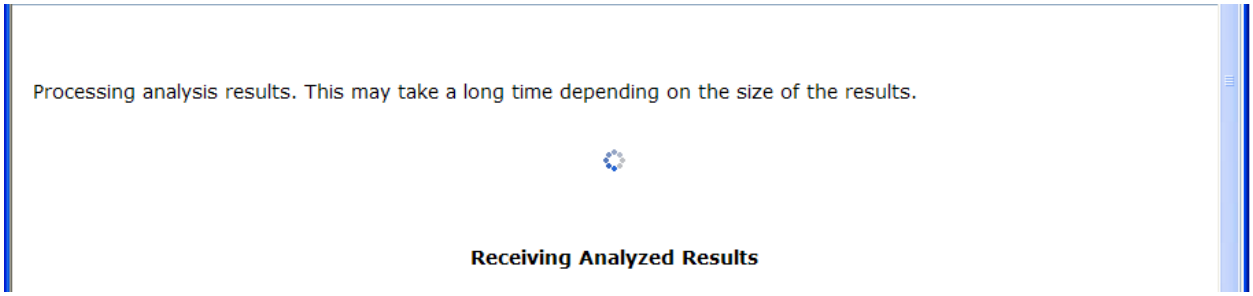


Figure 8 – Analysis processing update real time message

As the database is streaming the data to the chemistry analysis processors, processors will perform the analysis and start to display queried and processed results counts. When analysis processing is complete, the Analysis Results page is displayed with results of your analysis.

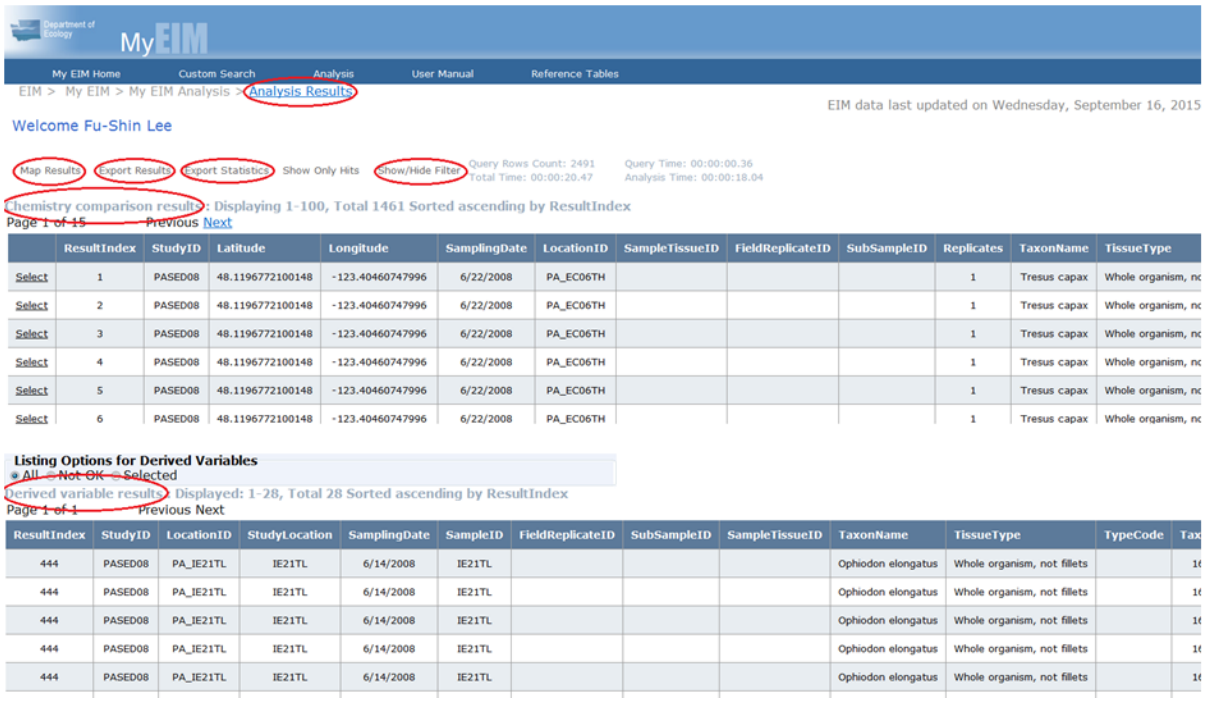


Figure 9 - Analysis Results page

That's it! With just a few clicks you have taken a data set and compared them with predefined standard cleanup criteria. The results of the analysis are laid out in two grids. The top grid is the Chemistry Analysis: Chemistry Comparison Results grid. Below this grid is a grid with derived variables calculation details.

Note: Derived variable calculation will be performed only when a selected standard had derived variables listed for comparison. When no cleanup parameter for derived variables is selected, analysis results page will show only aggregate chemistry comparison results at the top grid, and will not accompany derived variable calculation results below the top grid.

ANALYSIS RESULTS PAGE

Results are displayed on the screen through the Analysis Results page. From here you can map the analyzed results, filter the results down to a smaller subset of the full analyzed dataset, or export the results to a zipped comma separated values (CSV) file.

Each grid on this page provides paging through the data 100 rows at a time. This is done by clicking the Previous and Next buttons on the top of the grid. The total number of rows is displayed in the grid title.

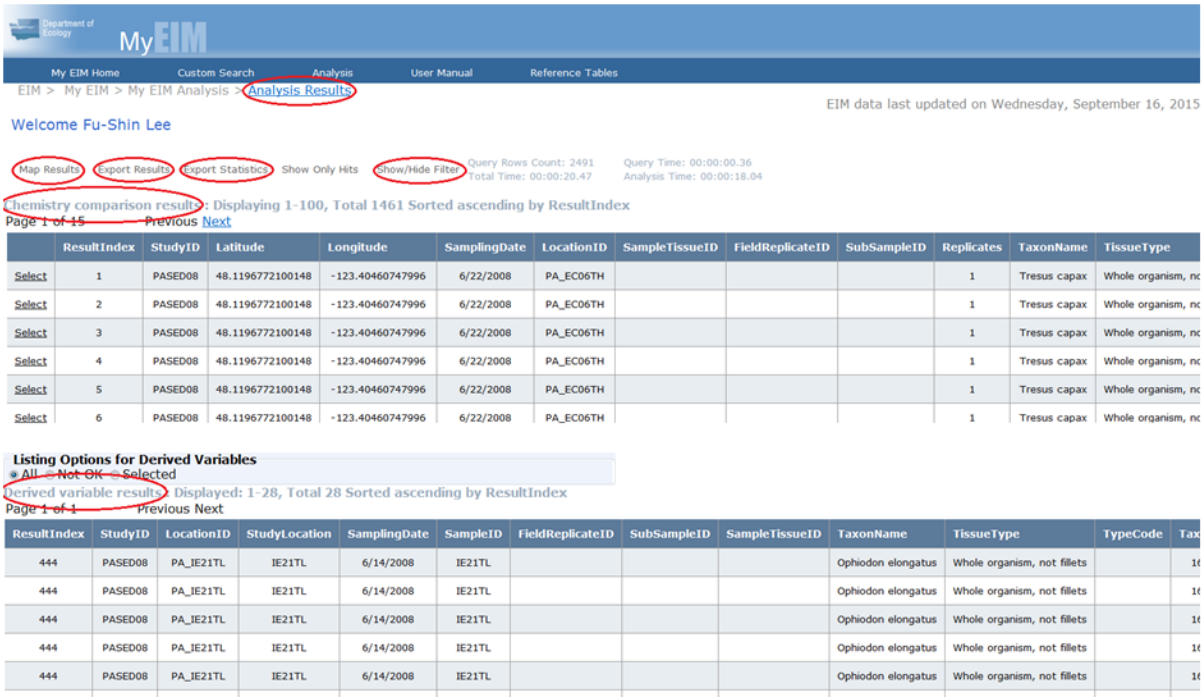


Figure 10 – Analysis Results page contains two grids: criteria comparison and derived variables.

The upper grid contains the criteria comparison results. Chemical concentrations at the chosen replicate level are aggregated using the data reduction logic explained in Appendix E, then normalized with respect to the unit of measure and measurement basis of the cleanup criteria before calculating the ratio (chemical concentration divided by criteria concentration) of concentration values to find Exceedance.

Some of the criteria in the system are defined using derived variables. Simple derived variables are calculated using the logic described Appendix F. TEQ weighted derived variables are calculated using the logic described in Appendix G.

CHEMISTRY COMPARISON RESULT GRID COLUMNS

	ResultIndex	StudyID	Latitude	Longitude	SamplingDate	LocationID	SampleTissueID	FieldReplicateID	SubSampleID	Replicates	TaxonName	TissueType
Select	1	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH				1	Tresus capax	Whole organism, nc
Select	2	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH				1	Tresus capax	Whole organism, nc
Select	3	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH				1	Tresus capax	Whole organism, nc
Select	4	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH				1	Tresus capax	Whole organism, nc
Select	5	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH				1	Tresus capax	Whole organism, nc
Select	6	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH				1	Tresus capax	Whole organism, nc

Figure 11a – First few columns of the comparison results grid with lab replicate level data reduction.

First few columns of comparison grid are shown in Figure 11a. The first column has all cells labeled "select". This is provides the link between the two grids. If the row contains a derived variable, clicking "select" on this row will filter the details of the derived variable and show it in the second grid. If the row is not a derived variable, then it will show an indicating message. Result Index column shows a unique identifier assigned for that row. This identifier is used to link this row for a derived variable detailed in the lower grid. By default this grid is sorted by Result Index column. All the other columns are reported values obtained from your custom search that identify the specific sample or aggregated sample except Replicates. Replicates shows the number of replicates aggregated at the Lab Replicate or Field Replicate Level.

TissueType	StudyLocation	SampleID	ChemicalName	CASNumber	CriteriaName	ChemicalConc	CriteriaConc	CriteriaUOM	CriteriaBasis	Exceedance	HitOrNot	Comment	Qualifier	LIPID	LipidNormConc
Whole organism, not exoskeleton or shell	EC06TH	EC06TH	1,2,3,7,8-PeCDF	57117-41-6	NR Fish_EPA3HHRBC2008_C	4.9E-08	8.1E-07	mg/kg	wet	0.06106		OK	U	0.985	5.015E-06
Whole organism, not exoskeleton or shell	EC06TH	EC06TH	1,2,4-trichlorobenzene	120-82-1	NR Fish_EPA3HHRBC2008_C	2	0.88	mg/kg	wet	2.283	Hit	OK	U	0.985	203
Whole organism, not exoskeleton or shell	EC06TH	EC06TH	1,2-dichlorobenzene	95-50-1	NR Fish_EPA3HHRBC2008_NC	2	120	mg/kg	wet	0.01639		OK	U	0.985	203
Whole organism, not exoskeleton or shell	EC06TH	EC06TH	1,4-dichlorobenzene	106-46-7	NR Fish_EPA3HHRBC2008_C	2	0.58	mg/kg	wet	3.425	Hit	OK	U	0.985	203
Whole organism, not exoskeleton or shell	EC06TH	EC06TH	1-Methylnaphthalene	90-12-0	NR Fish_EPA3HHRBC2008_C	2	0.11	mg/kg	wet	18.35	Hit	OK	U	0.985	203
Whole organism, not exoskeleton or shell	EC06TH	EC06TH	2,3,4,7,8-PeCDF	57117-31-4	NR Fish_EPA3HHRBC2008_C	7.3E-08	8.1E-08	mg/kg	wet	0.9023		OK	NJ	0.985	7.411E-06

Figure 11b – Sample, Chemical, Criteria Specific Comparison Columns in Chemistry Comparison Results Grid

Figure 11b shows the columns specific to each criteria comparison, Study Location Name, Sample ID, Chemical Name, CAS Number, Criteria Name, Chemical Concentration, Criteria Concentration, Criteria UOM, Criteria Basis, Hit or Not, Comment, Qualifier, Lipid and Lipid Normalized concentration. When the same chemical in multiple criteria are selected, the lowest criteria and criteria will be chosen to compare to the reported chemical concentrations normalized to the same UOM and basis as the criteria.

Criteria Name, Criteria Conc, Criteria UOM and Criteria Basis column values are imported from chosen criteria for chemicals in each row.

Chemical Conc column shows the calculated or aggregated or reported or concentration with the same measurement basis and unit of measure as the chosen criteria. For derived variables this will be derived variable value after unit of measure normalization. Calculated values of derived variables are used for comparing to criteria values where ever possible. If derived variable calculation was not possible for any reason and reported values of derived variable reported values are available in query data, MyEIM uses reported values for comparison.

Exceedance is the ratio of Chemical Conc to Criteria Conc.

HitOrNot column indicates if Chemical Conc is greater than the Criteria Value.

Comment column displays a message giving an explanation in case the calculation was unsuccessful or any non-default feature was used. In case this is a derived variable, the details of derived variable calculation are also imported here.

Qualifier column displays the qualifier code assigned to the chemical concentration after data reduction.

LIPID column shows the reported or an average of all LIPID values reported under replicate level data aggregation. LIPID values are shown only when LIPID data is queried as a part of the search data.

Columns are continued in Figure 11c.

ReportedConc	ReportedUOM	ReportedBasis	ReportingLimit	RLType	DetectionLimit	DLType	ReportedComment	ValidationLevel	AnalysisMethod	AnalysisLab
0.049	ng/Kg	wet	1.26	PQL	0.0494	MDL		QA1	EPA1613B	AXYS Analytical Services LTD, Sidney BC Canada
2000	ug/Kg	wet	2000	PQL	2000	MDL		QA1	SW8270	Analytical Resources Inc (ARI), Seattle WA
2000	ug/Kg	wet	2000	PQL	2000	MDL		QA1	SW8270	Analytical Resources Inc (ARI), Seattle WA
2000	ug/Kg	wet	2000	PQL	2000	MDL		QA1	SW8270	Analytical Resources Inc (ARI), Seattle WA
2000	ug/Kg	wet	2000	PQL	2000	MDL		QA1	SW8270	Analytical Resources Inc (ARI), Seattle WA
0.073	ng/Kg	wet	1.26	PQL	0.0494	MDL		QA1	EPA1613B	AXYS Analytical Services LTD, Sidney BC Canada

Figure 11c – Reported Concentration, RL, DL, Validation Level, Analysis Method and LabChemistry Comparison Results Grid.

Reported Conc column shows data reported reduced concentration value based on the data reduction rule chosen in preferences.

Reported UOM column shows unit of measure associated with the reported concentration.

Reported Basis column shows reported measurement basis for the chemical in the sample.

Reporting Limit, RL Type, Detection Limit, and DL Type are Result Reporting Limit, Result Reporting Limit Type, Result Detection Limit and Result Detection limit Type for the chemical in the sample reported by the Analysis Lab and Method from the search results.

Reported Comment show the comment for the reported results.

Validation Level shows the Result Validation Level for the chemical in the sample reported by the data validator following the data review and validation guidelines.

Analysis Method and Analysis Lab are the Result Method and Result Lab Name for the chemical in the sample from the chemistry search.

In case of no data reduction, the columns in Figure 11c show reported values from the chemistry search.

TaxonTSN	GeoLocation	QAPlanning	Assessment	Contact	Program	Location Setting	Study Type	StudyName
80955	17569184	4	See Results	Groven, Connie	ECY-TCP-SW	Marine	GenEnvironmentalStudy	Port Angeles Harbor Sediment Investigation.
80955	17569184	4	See Results	Groven, Connie	ECY-TCP-SW	Marine	GenEnvironmentalStudy	Port Angeles Harbor Sediment Investigation.
80955	17569184	4	See Results	Groven, Connie	ECY-TCP-SW	Marine	GenEnvironmentalStudy	Port Angeles Harbor Sediment Investigation.
80955	17569184	4	See Results	Groven, Connie	ECY-TCP-SW	Marine	GenEnvironmentalStudy	Port Angeles Harbor Sediment Investigation.
80955	17569184	4	See Results	Groven, Connie	ECY-TCP-SW	Marine	GenEnvironmentalStudy	Port Angeles Harbor Sediment Investigation.
80955	17569184	4	See Results	Groven, Connie	ECY-TCP-SW	Marine	GenEnvironmentalStudy	Port Angeles Harbor Sediment Investigation.

Figure 11d – Right Most columns in Chemistry Comparison Results Grid.

The right most columns of criteria comparison grid shown in Figure-11d are Taxonomic Serial Number (TSN), geolocation, Study QA Planning Level, Study QA Assessment Level, Ecology Contact, Ecology Program or Other Responsible Entity, Location Setting, Study Type and Study Name values from your chemistry search.

DERIVED VARIABLE GRID COLUMNS

Derived Variable grid is displayed only when data reduction at laboratory level is chosen. In cases where derived variables are calculated, the details of individual chemical constituents (from the top list) are listed in the middle derived variables grid. For example, if a criteria constituent of PCB is analyzed against a result containing PCB, the upper grid will display the summary of the evaluated concentration. The middle grid will contain 7 rows of data related to the result row in the upper grid because the PCB derived variable is defined with 7 constituents.

Listing Options for Derived Variables

◉ All ○ Not OK ○ Selected

Derived variable results : Displayed: 1-28, Total 28 Sorted ascending by ResultIndex

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Figure 12 –Filtering of Derived Variables

Filtering of the Derived Variable grid is possible three ways. These options are available between the upper and lower grids in the Listing Options for Derived Variables. Selecting All will display all derived variable results. Not OK will only display those derived variable values where the evaluation of the constituents could not be performed as desired, this will be reflected in the comments. The final option is Selected. This will display only those derived variables that match the selected row in the upper grid as shown in Figure 11b. The first column in the upper grid provides the link to display details of a derived variable in the lower grid.

Chemistry comparison results : Displaying 501-600, Total 1461 Sorted ascending by ResultIndex

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Select	530	PASED08	48.1349637778251	-123.454619700707	6/14/2008	PA_IE22TL				1	Ophiodon elongatus	Fillet, skin on
Select	531	PASED08	48.1349637778251	-123.454619700707	6/14/2008	PA_IE22TL				1	Ophiodon elongatus	Fillet, skin on
Select	532	PASED08	48.1349637778251	-123.454619700707	6/14/2008	PA_IE22TL				1	Ophiodon elongatus	Fillet, skin on
Select	533	PASED08	48.1349637778251	-123.454619700707	6/14/2008	PA_IE22TL				1	Ophiodon elongatus	Fillet, skin on
Select	**534**	**PASED08**	**48.1349637778251**	**-123.454619700707**	**6/14/2008**	**PA_IE22TL**				**1**	**Ophiodon elongatus**	**Fillet, skin on**
Select	535	PASED08	48.1349637778251	-123.454619700707	6/14/2008	PA_IE22TL				1	Ophiodon elongatus	Fillet, skin on
Select	536	PASED08	48.1349637778251	-123.454619700707	6/14/2008	PA_IE22TL				1	Ophiodon elongatus	Fillet, skin on

Listing Options for Derived Variables

○ All ○ Not OK ◉ Selected

Derived variable results : Displayed: 1-7, Filtered 7, Total 28 Sorted ascending by ResultIndex

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ResultIndex	StudyID	LocationID	StudyLocation	SamplingDate	SampleID	FieldReplicateID	SubSampleID	SampleTissueID	TaxonName	TissueType	TypeCode	TaxonTSN	DV Name
534	PASED08	PA_IE22TL	IE22TL	6/14/2008	IE22TL				Ophiodon elongatus	Fillet, skin on		167116	PCBs
534	PASED08	PA_IE22TL	IE22TL	6/14/2008	IE22TL				Ophiodon elongatus	Fillet, skin on		167116	PCBs
534	PASED08	PA_IE22TL	IE22TL	6/14/2008	IE22TL				Ophiodon elongatus	Fillet, skin on		167116	PCBs
534	PASED08	PA_IE22TL	IE22TL	6/14/2008	IE22TL				Ophiodon elongatus	Fillet, skin on		167116	PCBs
534	PASED08	PA_IE22TL	IE22TL	6/14/2008	IE22TL				Ophiodon elongatus	Fillet, skin on		167116	PCBs
534	PASED08	PA_IE22TL	IE22TL	6/14/2008	IE22TL				Ophiodon elongatus	Fillet, skin on		167116	PCBs

Figure 13a – Selected PCBs Derived Variables

First few columns as shown in Figure 14a are reported values obtained from your custom search that identify the specific tissue sample. Taxon Name, Tissue Type and Taxon TSN help to identify the specific tissue sample, as Upper Depth, Lower Depth and Depth UOM help to identify the specific sediment sample.

ResultIndex	StudyID	LocationID	StudyLocation	SamplingDate	SampleID	FieldReplicateID	SubSampleID	SampleTissueID	TaxonName	TissueType	TypeCode	TaxonTSN
444	PASED08	PA_IE21TL	IE21TL	6/14/2008	IE21TL				Ophiodon elongatus	Whole organism, not fillets		167116
444	PASED08	PA_IE21TL	IE21TL	6/14/2008	IE21TL				Ophiodon elongatus	Whole organism, not fillets		167116
444	PASED08	PA_IE21TL	IE21TL	6/14/2008	IE21TL				Ophiodon elongatus	Whole organism, not fillets		167116
444	PASED08	PA_IE21TL	IE21TL	6/14/2008	IE21TL				Ophiodon elongatus	Whole organism, not fillets		167116
444	PASED08	PA_IE21TL	IE21TL	6/14/2008	IE21TL				Ophiodon elongatus	Whole organism, not fillets		167116
444	PASED08	PA_IE21TL	IE21TL	6/14/2008	IE21TL				Ophiodon elongatus	Whole organism, not fillets		167116

Figure 14a –Few left most columns of the Derived Variable grid.

DV Name	DV Conc	DV UOM	DV Basis	DV Qualifier	Comment	ChemicalName	CASNumber	WeightedConc	%Contribution	LIPID	DLSF	Weight	ReportedConc	ReportedUOM	ReportedBasis	Reported Qualifier
PCBs	0.021	mg/Kg	wet		OK	aroclor 1016	12674-11-2	0.0032	0	2.34		1	0.0032	mg/Kg	wet	U
PCBs	0.021	mg/Kg	wet		OK	aroclor 1221	11104-28-2	0.0079	0	2.34		1	0.0079	mg/Kg	wet	U
PCBs	0.021	mg/Kg	wet		OK	aroclor 1232	11141-16-5	0.007	0	2.34		1	0.007	mg/Kg	wet	U
PCBs	0.021	mg/Kg	wet		OK	aroclor 1242	53469-21-9	0.0021	0	2.34		1	0.0021	mg/Kg	wet	U
PCBs	0.021	mg/Kg	wet		OK	aroclor 1248	12672-29-6	0.0013	0	2.34		1	0.0013	mg/Kg	wet	U
PCBs	0.021	mg/Kg	wet		OK	aroclor 1254	11097-69-1	0.0021	0	2.34		1	0.0021	mg/Kg	wet	U

Figure 14b –Columns specific to calculation details of the Derived Variable.

Columns named DV Name, DV UOM and DV basis show the information from the criteria based on which derived variables are calculated.

Calculated derived variable concentration is shown in DV Conc column.

DV qualifier shows the code assigned to the calculated value based on the derived variable calculation logic (please refer to appendices F and G).

Comment column indicates messages arising from calculation. 'OK' indicates that calculation is completed successfully with the complete set of individually reported constituent concentrations.

For every derived variable there are as many rows as its constituent chemicals, one for each chemical. Chemical Name column indicates name of the constituent.

CAS Number is the Chemical Abstracts Service number of the chemical constituent.

Weighted Conc shows the concentration of the chemical after normalizing with respect to unit of measure and measurement basis of selected criteria if necessary, and scaled by detection limit scaling factor (DLSF) if non-detect as indicated by the U or U containing qualifier under Report Qualifier column and scaled by weights as assigned in the definition of the derived variable in the criteria.

%Contribution column shows the contribution of this weighted concentration to the total sum that makes up derived variable concentration (DV Conc).

LIPID shows the reported or an average of all LIPID values reported under replicate level data aggregation. LIPID values are shown only when LIPID data is queried as a part of the search data.

Detection Limit Scaling Factor and weight for each chemical originate from the definition of the derived variable in the criteria.

Figure 14c shows the columns specific to the reported Result values of the chemical and the sample.

Reported Conc shows the reported concentration from search results or the data reduced value of the chemical concentration, if the sample has laboratory replicates.

Reported UOM and Reported basis originate from search results.

Reported Qualifier is the qualifier code arising from data reduction or reported value.

ReportedConc	ReportedUOM	ReportedBasis	Reported Qualifier	ReportingLimit	RLType	DetectionLimit	DLType	ReportedComment	ValidationLevel	AnalysisMethod	AnalysisLab
0.0032	mg/Kg	wet	U	0.0099	PQL	0.0032	MDL		QA1	SW8082	TestAmerica, Tacoma WA (7/1/07-1/25/10, see lab detail for current info)
0.0079	mg/Kg	wet	U	0.0099	PQL	0.0079	MDL		QA1	SW8082	TestAmerica, Tacoma WA (7/1/07-1/25/10, see lab detail for current info)
0.007	mg/Kg	wet	U	0.0099	PQL	0.007	MDL		QA1	SW8082	TestAmerica, Tacoma WA (7/1/07-1/25/10, see lab detail for current info)
0.0021	mg/Kg	wet	U	0.0099	PQL	0.0021	MDL		QA1	SW8082	TestAmerica, Tacoma WA (7/1/07-1/25/10, see lab detail for current info)
0.0013	mg/Kg	wet	U	0.0099	PQL	0.0013	MDL		QA1	SW8082	TestAmerica, Tacoma WA (7/1/07-1/25/10, see lab detail for current info)
0.0021	mg/Kg	wet	U	0.0099	PQL	0.0021	MDL		QA1	SW8082	TestAmerica, Tacoma WA (7/1/07-1/25/10, see lab detail for current info)

Figure 14c – Columns specific to reported values of the chemical and the sample.

Reporting Limit, RL Type, Detection Limit, and DL Type are Result Reporting Limit, Result Reporting Limit Type, Result Detection Limit and Result Detection limit Type for the chemical in the sample reported by the Analysis Lab and Method from the search results.

Reported Comment show the comment for the reported results.

Validation Level shows the Result Validation Level for the chemical in the sample reported by the data validator following the data review and validation guidelines from the search results.

Analysis Method and Analysis Lab are the Result Method and Result Lab Name for the chemical in the sample from the chemistry search results.

Study Type	Location Setting	QAPlanning	Assessment	Contact	Program	StudyName
GenEnvironmentalStudy	Marine	4	See Results	Groven, Connie	ECY-TCP-SW	Port Angeles Harbor Sediment Investigation.
GenEnvironmentalStudy	Marine	4	See Results	Groven, Connie	ECY-TCP-SW	Port Angeles Harbor Sediment Investigation.
GenEnvironmentalStudy	Marine	4	See Results	Groven, Connie	ECY-TCP-SW	Port Angeles Harbor Sediment Investigation.
GenEnvironmentalStudy	Marine	4	See Results	Groven, Connie	ECY-TCP-SW	Port Angeles Harbor Sediment Investigation.
GenEnvironmentalStudy	Marine	4	See Results	Groven, Connie	ECY-TCP-SW	Port Angeles Harbor Sediment Investigation.
GenEnvironmentalStudy	Marine	4	See Results	Groven, Connie	ECY-TCP-SW	Port Angeles Harbor Sediment Investigation.

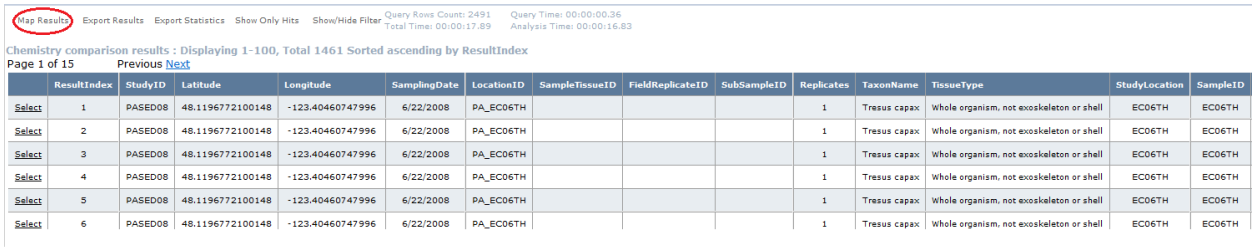
Figure 14d – Right Most columns in Derive Variables Grid.

Study Type, Location Setting, QA Planning, Assessment, Contact, Program, and Study Name in Figure 14d show reported values for Study Type, Location Setting, Study QA Planning Level, Study QA Assessment Level, Ecology Contact, Ecology Program or Other Responsible Entity, and Study Name from the search results.

EXERCISE 2: MAP RESULTS

(1) Run the Tissue Query you have saved and compare to tissue criteria for carcinogens. The analyzed results can be mapped to show where chemical concentrations exceeded the selected Comparison Criteria. This is done by clicking the Map Results link.

(2) Click on "Map Results".



	ResultIndex	StudyID	Latitude	Longitude	SamplingDate	LocationID	SampleTissueID	FieldReplicateID	SubSampleID	Replicates	TaxonName	TissueType	StudyLocation	SampleID
Select	1	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH				1	Tresus capax	Whole organism, not exoskeleton or shell	EC06TH	EC06TH
Select	2	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH				1	Tresus capax	Whole organism, not exoskeleton or shell	EC06TH	EC06TH
Select	3	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH				1	Tresus capax	Whole organism, not exoskeleton or shell	EC06TH	EC06TH
Select	4	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH				1	Tresus capax	Whole organism, not exoskeleton or shell	EC06TH	EC06TH
Select	5	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH				1	Tresus capax	Whole organism, not exoskeleton or shell	EC06TH	EC06TH
Select	6	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH				1	Tresus capax	Whole organism, not exoskeleton or shell	EC06TH	EC06TH

Figure 15–Map Results link

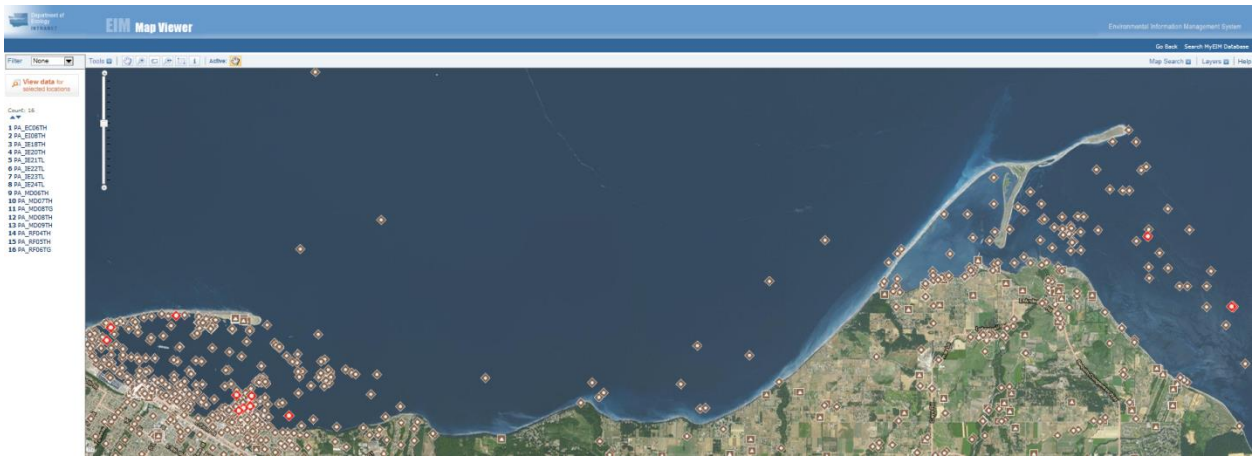


Figure 16 - Mapped analysis results for PASED08 study tissue samples.

When results are mapped, concentration values from samples taken which exceed the concentration value of a selected standard, the resulting dot on the map is automatically highlighted in Red.

EXERCISE 3: EXPORT RESULTS

Selecting the Export Results link will allow you to download the analyzed results as a CSV file. This file can then be opened in a spreadsheet program such as Microsoft Excel.

(1) Click on the Export Results link.

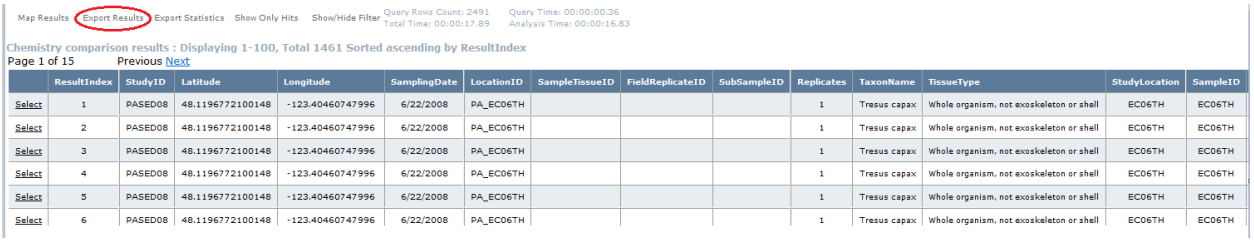


Figure 17 - Export Results link

A dialog box prompt will confirm the file download. Click Open or Save. Click Open in Figure 18a to bring you to the zip file in Figure 18b. This zip file will contain two spreadsheet files, chemistry comparison results at the top grid and derived variable results at the middle grid on Analysis Results page. You can double click on the files in Figure 18b to view and save these spreadsheets in your folder.

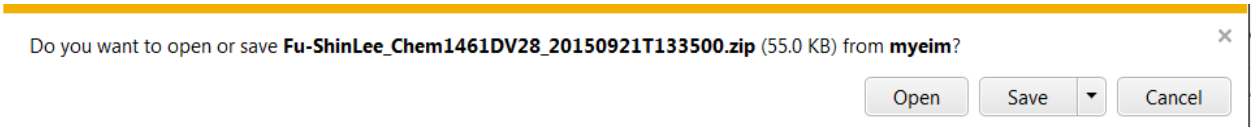


Figure 18a - Export results dialog box.

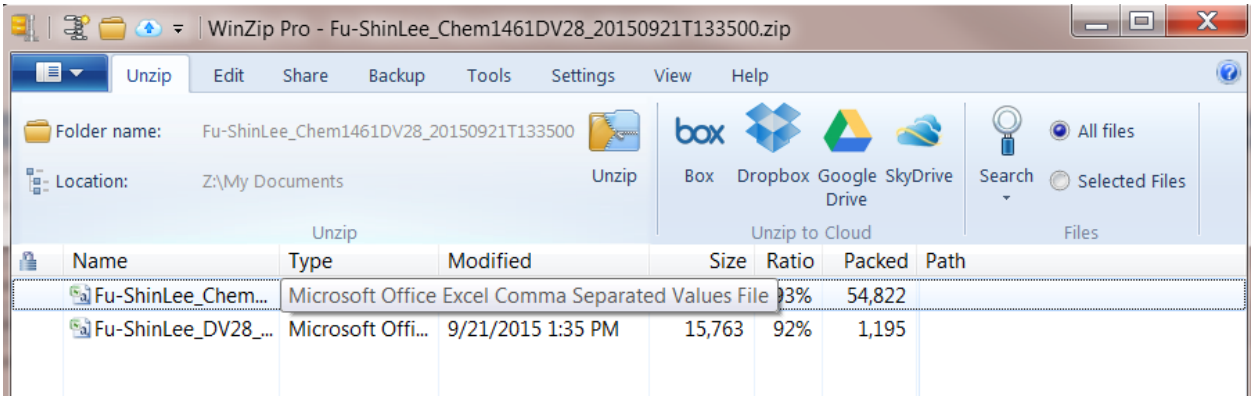
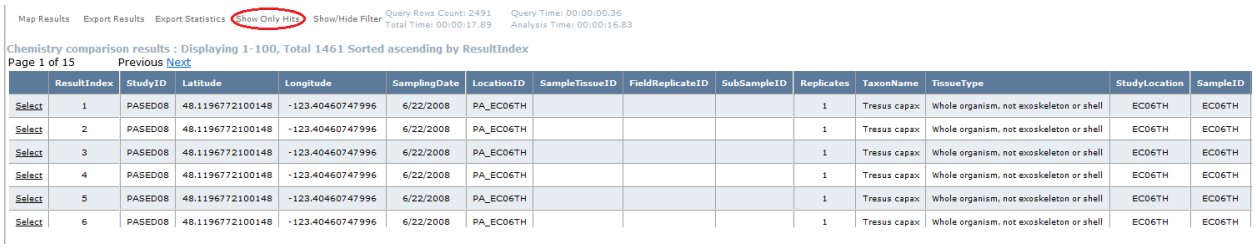


Figure 18b - Export results in Zip File.

EXERCISE 4: SHOW ONLY HITS

The Show Only Hits link will filter the Comparison Results grid to show only those chemicals that exceed the selected standards.

(1) Click on the 'Show Only Hits' link.



Map Results Export Results Export Statistics Show Only Hits Show/Hide Filter Query Rows Count: 2491 Total Time: 00:00:17.89 Query Time: 00:00:00.36 Analysis Time: 00:00:16.83

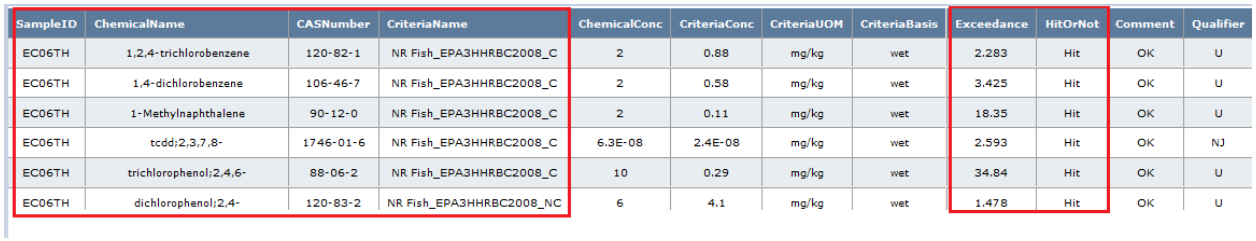
Chemistry comparison results : Displaying 1-100, Total 1461 Sorted ascending by ResultIndex

Page 1 of 15 Previous Next

	ResultIndex	StudyID	Latitude	Longitude	SamplingDate	LocationID	SampleTissueID	FieldReplicateID	SubSampleID	Replicates	TaxonName	TissueType	StudyLocation	SampleID
Select	1	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH				1	Tresus capax	Whole organism, not exoskeleton or shell	EC06TH	EC06TH
Select	2	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH				1	Tresus capax	Whole organism, not exoskeleton or shell	EC06TH	EC06TH
Select	3	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH				1	Tresus capax	Whole organism, not exoskeleton or shell	EC06TH	EC06TH
Select	4	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH				1	Tresus capax	Whole organism, not exoskeleton or shell	EC06TH	EC06TH
Select	5	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH				1	Tresus capax	Whole organism, not exoskeleton or shell	EC06TH	EC06TH
Select	6	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH				1	Tresus capax	Whole organism, not exoskeleton or shell	EC06TH	EC06TH

Figure 19 - Show Only Hits link

(2) Notice that only the chemicals exceeding the lowest selected cleanup criteria are displayed.



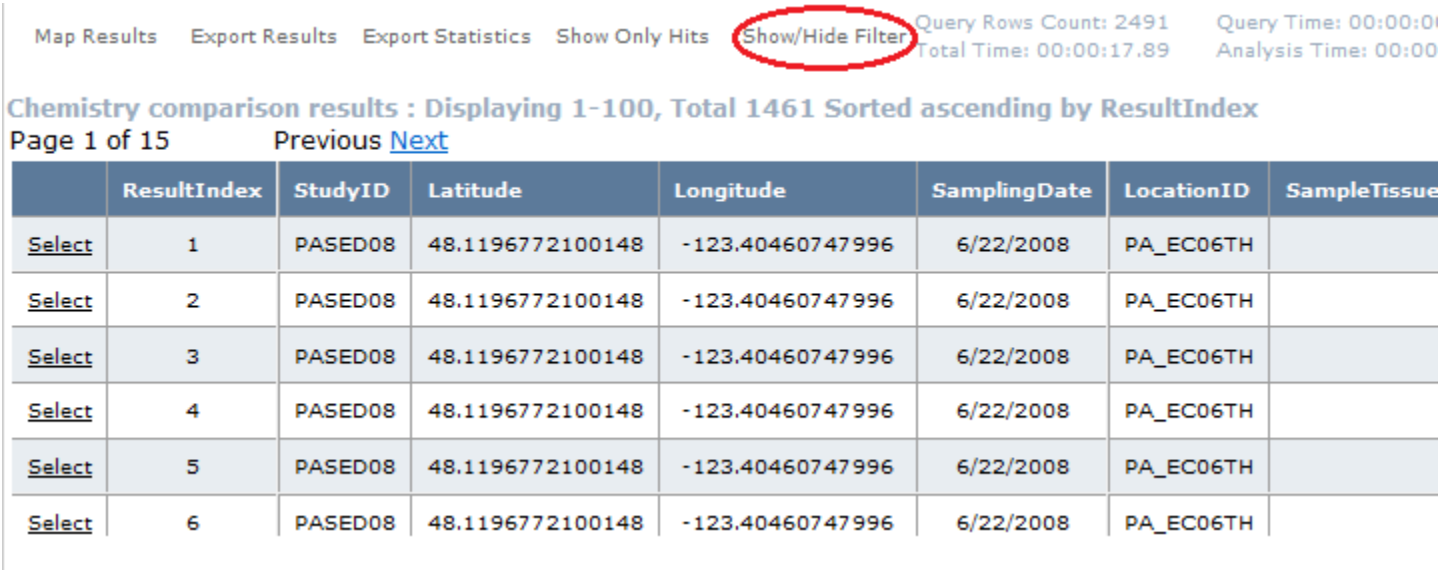
SampleID	ChemicalName	CASNumber	CriteriaName	ChemicalConc	CriteriaConc	CriteriaUOM	CriteriaBasis	Exceedance	HitOrNot	Comment	Qualifier
EC06TH	1,2,4-trichlorobenzene	120-82-1	NR Fish_EPA3HHRBC2008_C	2	0.88	mg/kg	wet	2.283	Hit	OK	U
EC06TH	1,4-dichlorobenzene	106-46-7	NR Fish_EPA3HHRBC2008_C	2	0.58	mg/kg	wet	3.425	Hit	OK	U
EC06TH	1-Methylnaphthalene	90-12-0	NR Fish_EPA3HHRBC2008_C	2	0.11	mg/kg	wet	18.35	Hit	OK	U
EC06TH	tcdd;2,3,7,8-	1746-01-6	NR Fish_EPA3HHRBC2008_C	6.3E-08	2.4E-08	mg/kg	wet	2.593	Hit	OK	NJ
EC06TH	trichlorophenol;2,4,6-	88-06-2	NR Fish_EPA3HHRBC2008_C	10	0.29	mg/kg	wet	34.84	Hit	OK	U
EC06TH	dichlorophenol;2,4-	120-83-2	NR Fish_EPA3HHRBC2008_NC	6	4.1	mg/kg	wet	1.478	Hit	OK	U

Figure 20 - Result data exceeding the standard.

EXERCISE 5: SHOW/HIDE FILTER

Selecting the Show/Hide Filter link will allow you place filtering constraints on the analyzed data you are viewing. Previous exercise in fact processed a predefined filter to look for hits.

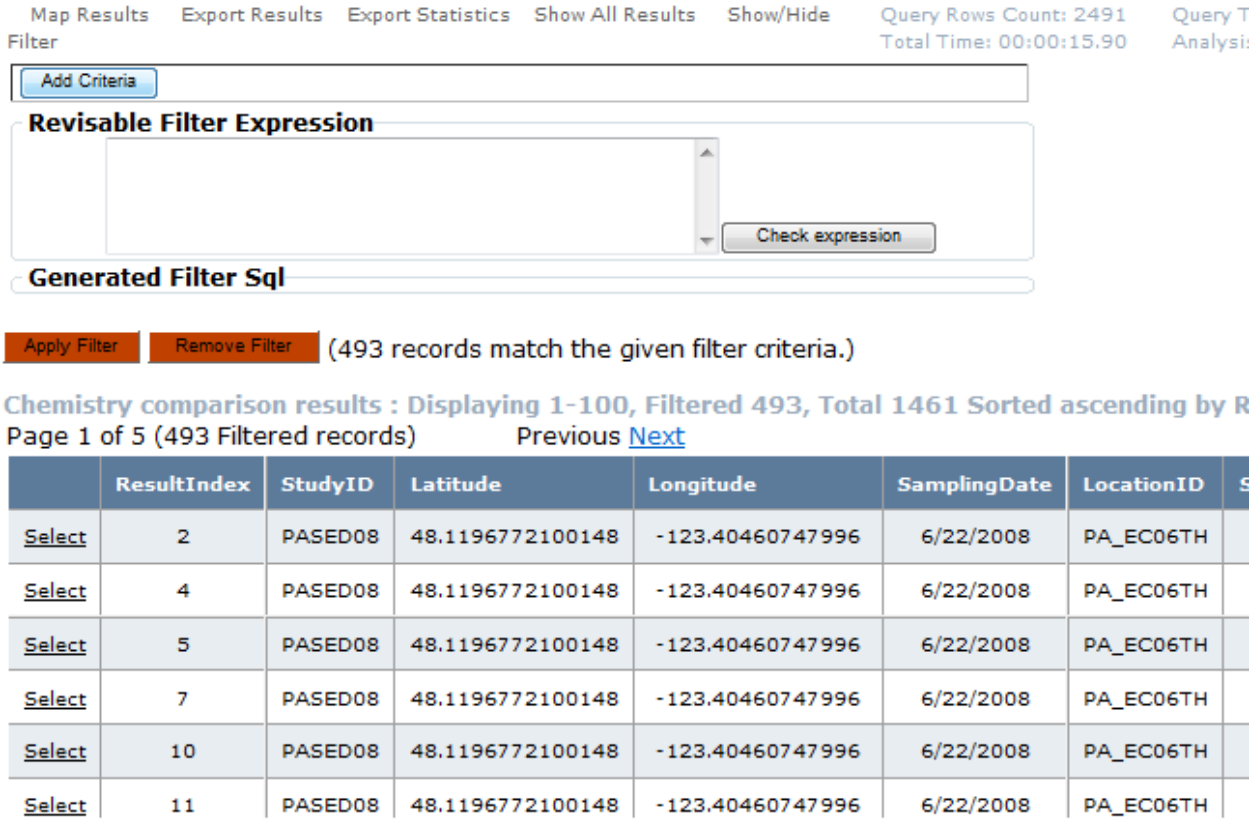
(1) Click on the Show/Hide Filter link.



	ResultIndex	StudyID	Latitude	Longitude	SamplingDate	LocationID	SampleTissue
Select	1	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH	
Select	2	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH	
Select	3	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH	
Select	4	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH	
Select	5	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH	
Select	6	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH	

Figure 21 - Show/Hide filter link

(2) The filter appears. The Filter control allows you to set constraints on the results in the grid.



	ResultIndex	StudyID	Latitude	Longitude	SamplingDate	LocationID
Select	2	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH
Select	4	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH
Select	5	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH
Select	7	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH
Select	10	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH
Select	11	PASED08	48.1196772100148	-123.40460747996	6/22/2008	PA_EC06TH

Figure 22 - Filter control becomes visible above the comparison results.

The filter control used here works just like the Custom Search filter control. To begin, click on the 'Add Criteria' button. A new filter row will be displayed.

(3) Select ChemicalName under 'Field Name' and Equal under 'Operator'. Start to type PCB-126 and select from the displayed suggestions. Select TaxonlName under 'Field Name' and Equal under 'Operator'. Click on 'Update'. Start to type Tresus capax and select from the displayed suggestions. Clicking on 'Update', and 'Apply Filter'in Figure 23. 'Map Results' will bring you to the PCB-126 tresus capax red hit and blue pass stations in Figures 23.

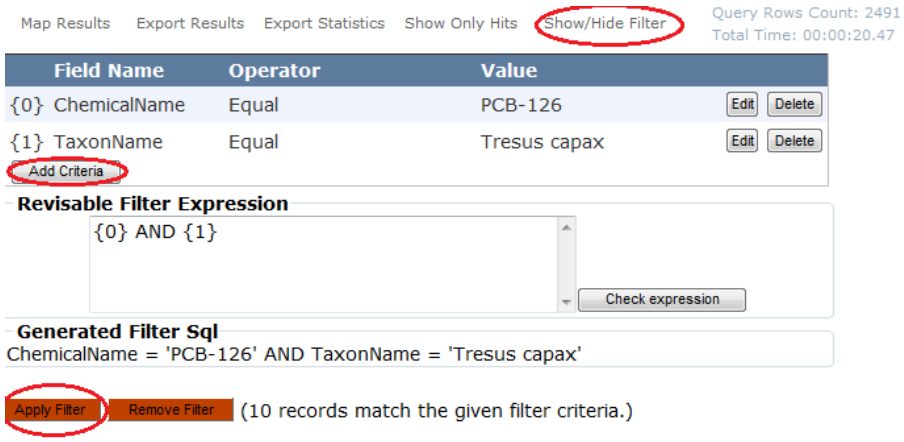


Figure 23 – The Custom Filter Control

(4) Clicking on 'Map Results' will bring you to the PCB-126 tresus capax red hit and blue pass stations in Figures 24.

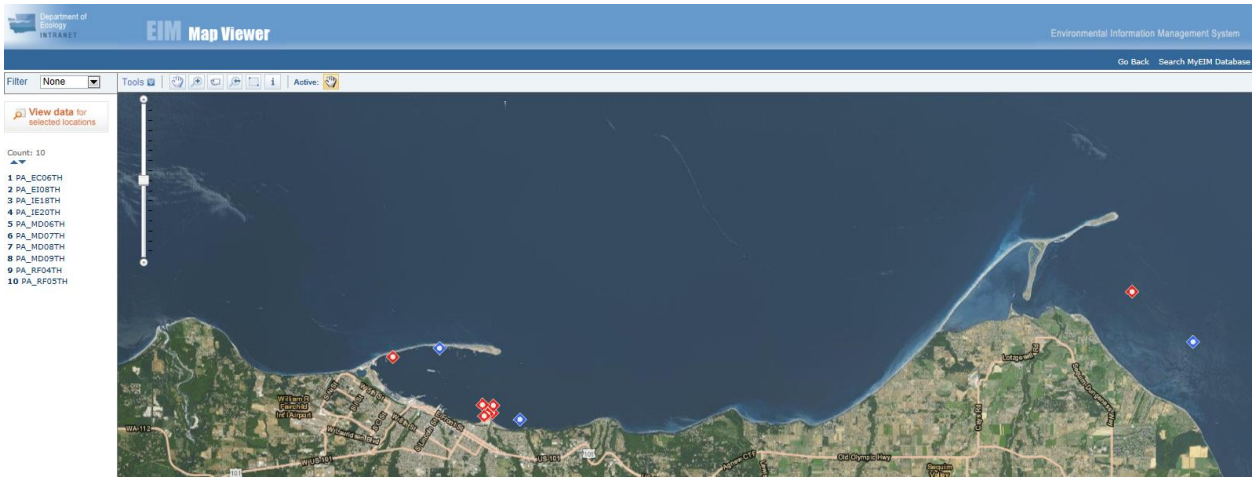


Figure 24 – EIM Map Viewer Page for Analyzed PCB-126 Tresus capax Chemistry Results

Comparing the maps in Figures 16 and 24 would give you the information on how much PCB-126 in tresus capax contribute to the hit stations in relation to all the chemistry comparison result hits for all species, tissue types, and chemicals. PCB-126 were chosen, because it was identified as one of potential indicator hazardous substances in the statistical summary spreadsheet.

Note: When you Export Results, the exported files will contain only the filtered results. When you Map Results only the filtered results show up in the Map.

The filter tool operates on the Chemistry Analysis results grid. The Derived Variable grid is filtered through the radio buttons shown in Listing Options for Derived Variables and using "select" link provided at the beginning of each row in the Chemistry Analysis results grid.

Results can be sorted based on column values in the chemistry results as well as derived variables grids by clicking on the column header which needed to be sorted. Sorting can be done with or without applying the filters. If the column values are associated with values in the other columns, MyEIM sorting algorithm takes this factor into account. For example, since concentrations are associated with unit of measure, MyEIM sorts concentrations by taking into account the unit of measure. Similarly upper depth and lower depth values are sorted using depth unit of measure.

Note: Sort and filter the output feature in MyEIM is especially useful if the sorted/filtered column is dependent on another column as in the above example. In Excel you will need to write a custom sorting/filtering macro or code to achieve the same result.

CUSTOMIZING YOUR ANALYSIS

Eventually, you may want to define cleanup criteria of your own with chemicals and criteria values different from those found in the Standard Cleanup Criteria list. MyEIM analysis allows you to create “User Defined Cleanup Criteria” by either copying existing standard criteria or, by creating new criteria.

If you copy existing criteria you can always alter it. If you defined new criteria, you can add constituents to it. You can delete or modify each of the constituents.

There are three types of constituents: chemicals, derived variables and user defined derived variables. Complete lists of chemicals and standard derived variables are already available in MyEIM for you to choose from.

You can define your own customized derived variables and add them to criteria list. In this section you will learn to create user defined criteria and user defined derived variables.

EXERCISE 6: CREATING CUSTOM CLEANUP CRITERIA

(1) Let's use the 'Analysis' link through MyEIM Home page to navigate to the criteria page. Open MyEIM in a new browser window and Click on Analysis Link.

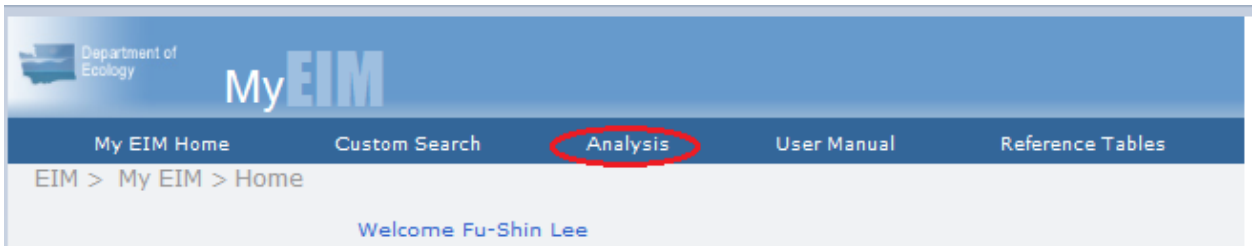


Figure 25 – Link at MyEIM Home Page to Cleanup Criteria page.

(2) In the 'Analysis Home' page, click on Chemistry Criteria.

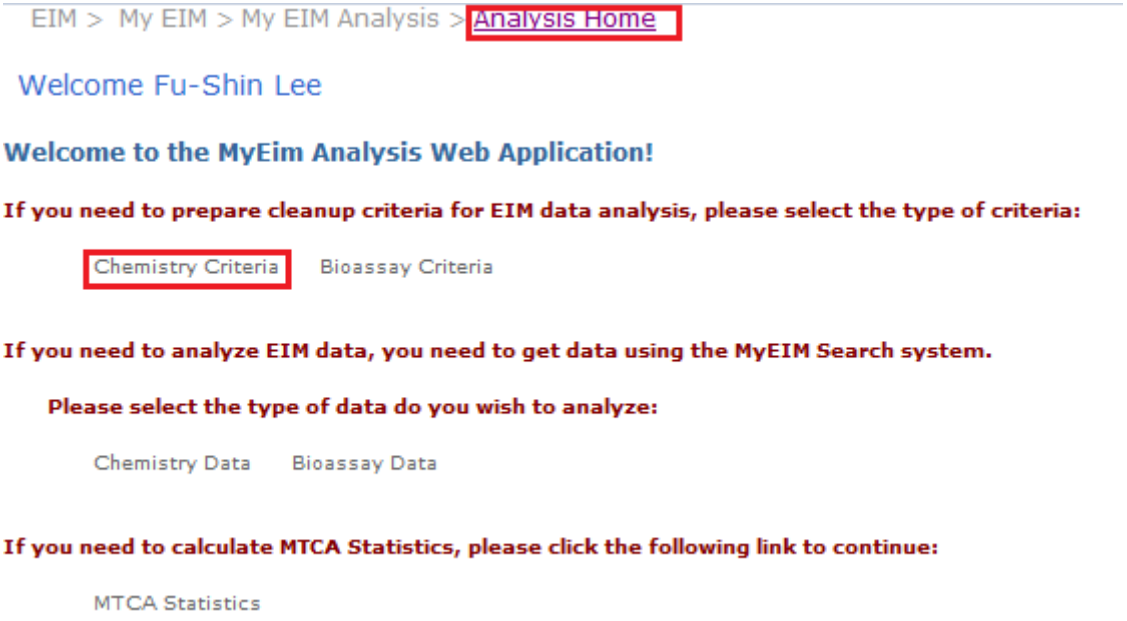


Figure 26 – MyEIM Analysis Home Page.

(3) From the Choose Comparison Criteria page, select the User Defined Cleanup Criteria tab. If this is the first time you've clicked this tab, a message informs you to "Please make a copy of the Standard Cleanup Criteria that you want to see in this tab or Add a new one...." Notice how no criteria are listed.

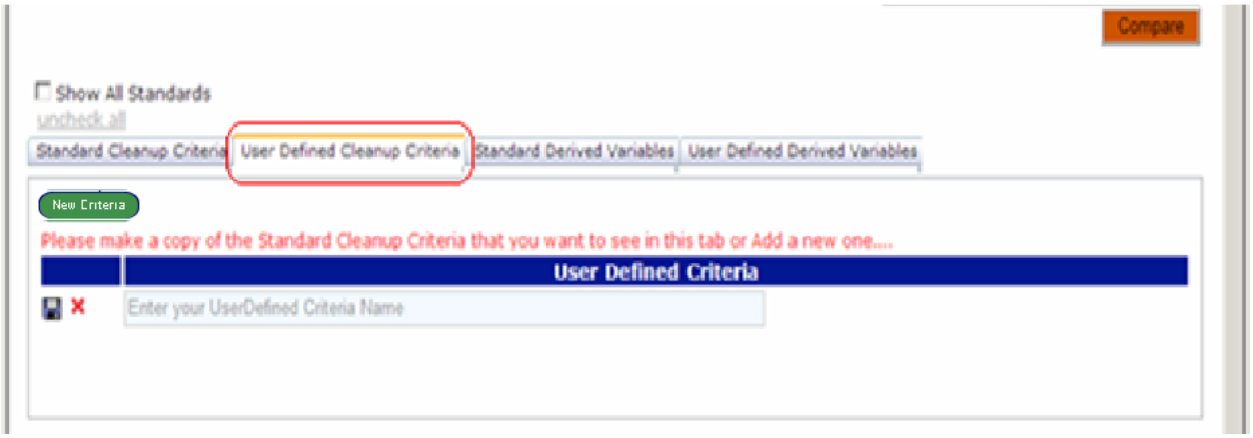


Figure 27 - Empty User Defined Cleanup Criteria

(4) If there were no cleanup parameters created before, MyEIM will prompt you to create a new one. If you go back to the first Cleanup Criteria tab. To the right of each list item is a Copy button . Clicking the Copy button creates a copy of the definition under your profile for modification. If you have already created criteria before, click on the green button "New Criteria" to add new criteria.

(5) Let us create a new criteria set from fresh. Give your new criteria a name "Tissue Criteria"

Figure 28 –Name to new Cleanup Criteria

Save by clicking on the floppy icon .

(6) MyEIM will prompt you to input the constituents. Select Chemical in the Constituent Type, Arsenic as constituents, UOM as ug/kg, 'wet' basis and a concentration of 0.62. You may also add optional comment.

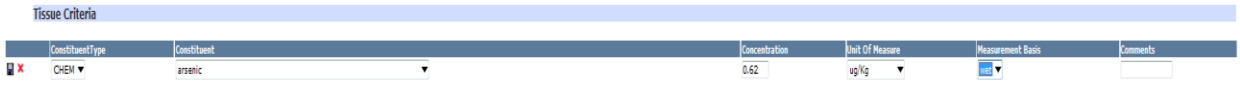


Figure 29 – New cleanup parameter added for arsenic.

(7) Add another cleanup parameter by clicking on the green ‘Add Constituent’ button.

Figure 30 – Adding another cleanup parameter

(8) Add another cleanup parameter, derived variable PCBs by clicking on the green ‘Add Constituent’ button.

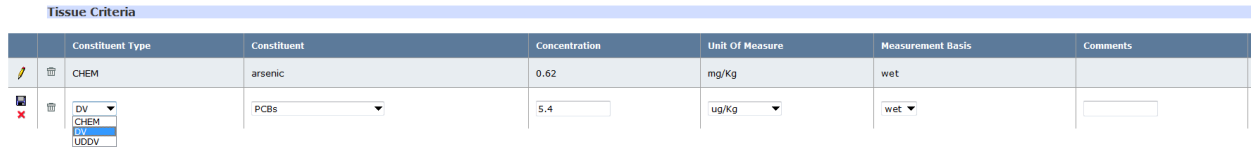


Figure 31 – Add another cleanup parameter, a derived variable.

When a user defined criteria is selected, its constituents are listed in the grid below. Each constituent can be edited by clicking on the pencil image. The pencil image disappears and is replaced by a Save disk image and a Cancel red X image. You’ll notice there is also a Delete trash can image. After making your change, be sure to select Save.

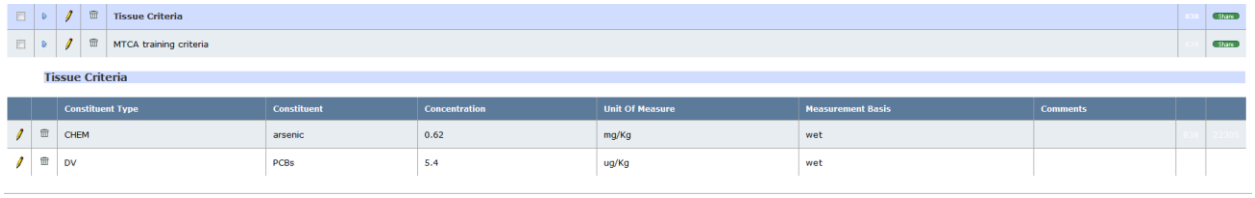


Figure 32 – Constituent cleanup parameters of your customized criteria.

(9) Once you are satisfied with the constituent list, you can select the User Defined Cleanup Criteria just as you would select a Standard Criteria to compare to your searched data of interest. The selected Tissue Criteria is shown in the Selected Standards box in Figure 33.

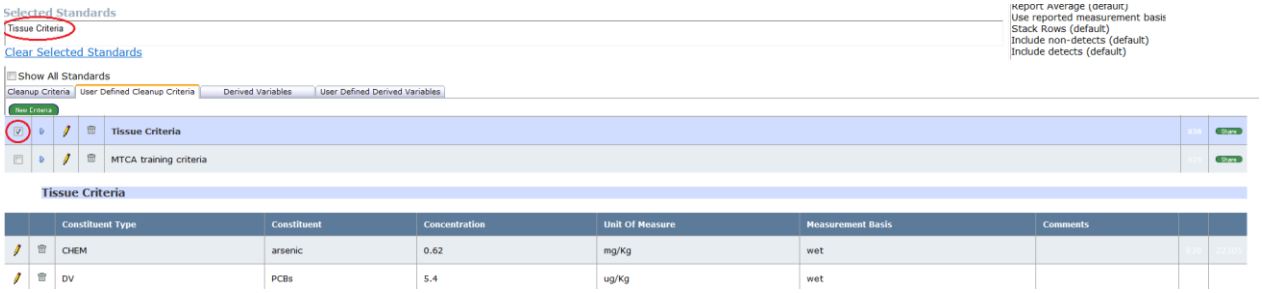


Figure 33 - User Defined Cleanup Criteria selected for comparison.

(10) When you click Compare, your custom User Defined Cleanup Criteria will be used used to compare to your searched and calculated data of interest as shown in Figure 34

Figure 34 – User Defined Cleanup Criteria used for comparison.

EXERCISE 7: CREATING A CUSTOM DERIVED VARIABLE

(1) Click the User Defined Derived Variables tab. A message instructs you to "Please make a copy of the Standard derived variable that you want to see in this tab…" and a blank user defined derived variable is open and prompting you to defined. Just like the Cleanup Criteria, you can either copy an existing derived variable and alter it, or create a new one from fresh.

(2) To Copy and alter an existing Derived Variable: Go to the Standard Derived Variables tab.

To the right of each list item is a Copy image  . Clicking the Copy button creates a copy of the definition under your profile for modification.

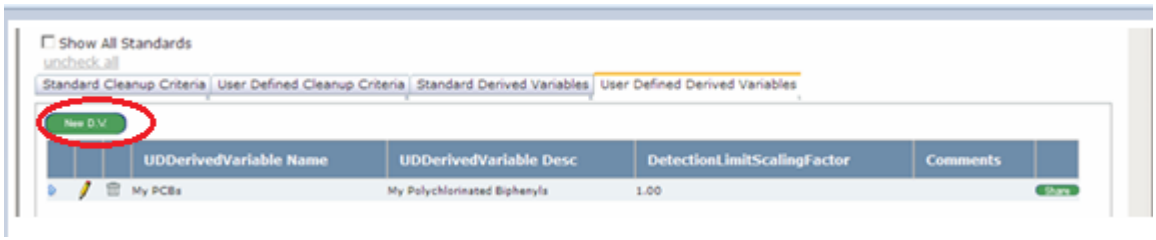


Figure 35- User Defined Derived Variables

(3) To Create a New Derived Variable: Click the green "New D.V." button in the User Defined Derived Variable tab if a new derived variable isn't already open. In the "UDDerivedVariable Name" column, simply enter a name for the new derived variable. Give it a "Detection Limit Scaling Factor" value, and optional comments. Click the disk icon to save.

Figure 36 - Empty User Defined Derived Variables

The Detection Limit Scaling Factor scales non-detect reported values. If the constituent chemical is a non-detect, then its reported value will be normalized to the unit of measure, normalized to measurement basis if required, scaled down by detection limit scaling factor, multiplied by the weight (toxicity equivalency factor for TEQ) and then added to the total derived Variable Value. Allowed value is in the range 0 <= 'Detection Limit Scaling Factor' <=1.

The new entry has three actions that you can perform. Each is represented by an icon. The name of the new User Defined Derived Variable can be modified by clicking the pencil icon. Change the name to something meaningful and click the Save icon. In this case the name was changed to "Tissue cPAH-TEQ"

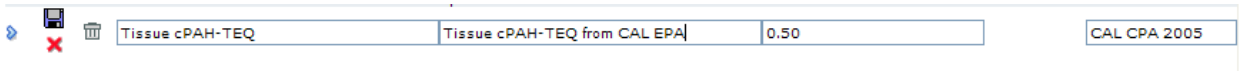


Figure 37 - User Defined Derived Variable in Edit Mode

(4) The blue arrow symbol selects the item and displays the constituents in a list. Clicking the green "New Constituent" button will open a new row in edit mode. Simply select a chemical from the drop-down list and assign a weight.

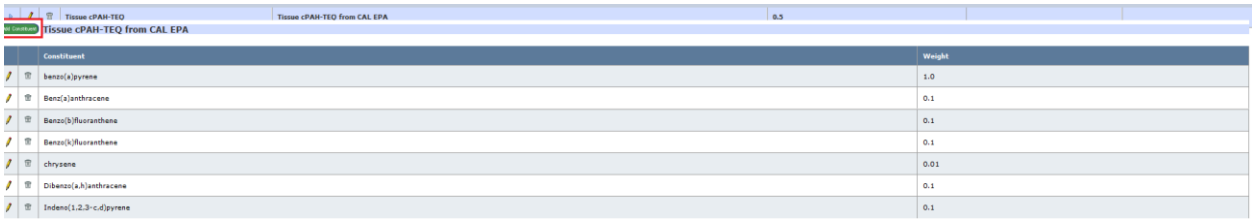


Figure 38- Constituents listed for a user defined derived variable

Each constituent can be edited by clicking on the pencil image. The pencil image disappears and is replaced by a Save disk image, a Cancel red X image, and a Delete trash can image. After making your changes a shown in Figure 39, select the Save or Cancel image to save or cancel your edit.

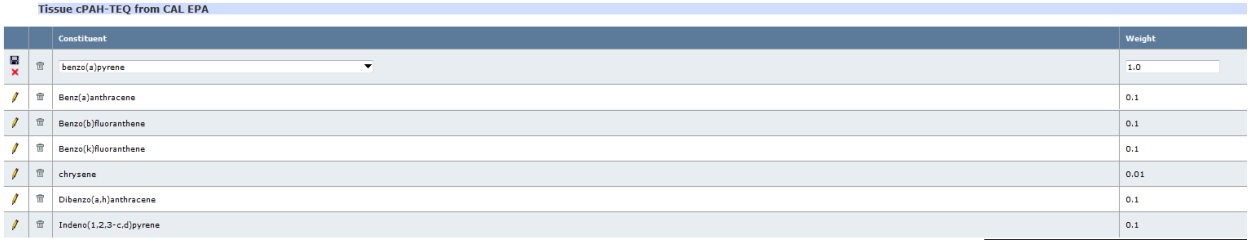


Figure 39- Constituents edited for a user defined derived variable

EXERCISE 8: CREATING A CUSTOM CRITERIA

You will need to add the derived variable you defined in the previous exercise in order to calculate it and compare to a criteria value of your own.

(1) To use your custom derived variable in analysis, switch over to the User Defined Cleanup Criteria tab. Expand "Tissue Criteria" using blue arrow. Click on green Add Constituent button.

(2) In the Constituent Type drop-down, select "UDDV" and then select the custom derived variable you just created from the constituent drop-down.

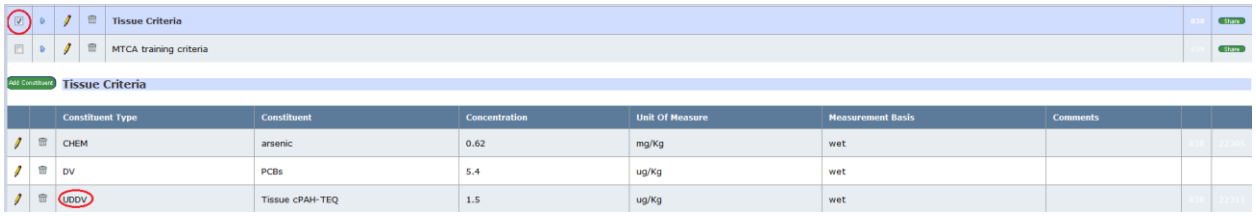


Figure 40 - Selecting a User Defined Derived Variable for a custom analysis.

Set the other properties (Unit of Measure, Measurement Basis, and Concentration) and then save the constituent.

(3)Then check the checkbox to the left of the cleanup criteria and click the orange "Compare" button.

(4) Your custom derived variable will be calculated and compared with your criteria concentration value. Let us create a custom query for Study ID = PASED08

ID	Category	Field Name	Operator	Value	
{0}	Sample	Sample Source	Equal	Animal Tissue	Edit Delete
{1}	Study	Study ID	Equal	PASED08	Edit Delete

Figure 41 –Custom query to test user defined criteria

(5) Select the Tissue criteria and compare.

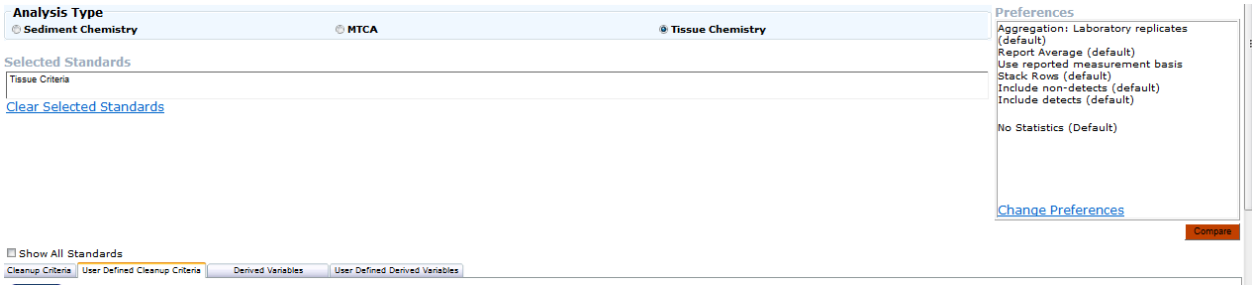


Figure 46 –Custom query to test user defined criteria

(6) You have successfully created your custom criteria and used it to analyze tissue data.

Figure 47–Results of custom derived variables in custom criteria

Chapter 8: Soil and Water Chemistry Analysis

The MyEIM Analysis application provides the tools to perform criteria comparison and statistical analysis of soil and water chemistry results queried through the quick start search in Search Templates or your saved search in My Custom Searches or chemistry search in Custom Search.

OVERVIEW OF SOIL AND WATER CHEMISTRY ANALYSIS

The MyEIM Analysis application provides tools to compare the searched results of interest to selected cleanup standards (also known as cleanup criteria). All CLARC cleanup standards for soil and water are available under 'Cleanup Criteria' tab in MyEIM. Users are not restricted to compare searched results to predefined cleanup standards. MyEIM Analysis provides an interface for you to define your own set of standards and derived variables using user defined cleanup criteria and user defined derived variables.

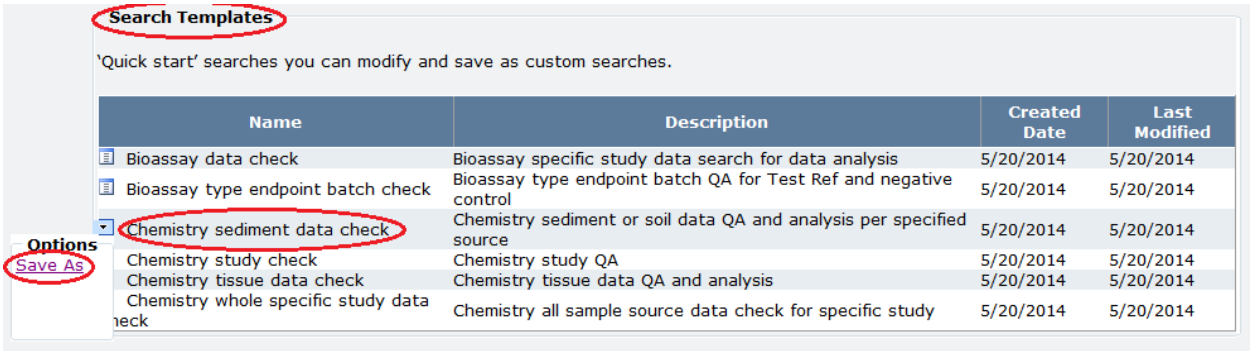
This chapter consists of three sections: Soil or/and Water Chemistry Data Search, Standard Analysis, and Customizing My Analysis. Soil or/and Water Chemistry Data Search will show you the steps necessary to perform in preparation for data analysis. Standard Analysis will cover the use of predefined cleanup criteria as the basis of analysis. Customizing My Analysis will discuss various user definable aspects of the application. Several exercises will help demonstrate the use of the various features.

Note: This chapter assumes you already know how to acquire data result sets using the Search application. If you need to review how to search EIM data and prepare a result set to work with, please refer to the Home and Search chapters.

SOIL OR/AND WATER CHEMISTRY DATA SEARCH

To begin the analysis process, you will first have to get a result set from the quick start search template (Chemistry sediment data check) in Search Templates or your saved search in My Custom Search or chemistry search in Custom Search.

Note: If you need a soil chemistry result set to get started, select 'Chemistry sediment data check' in Search Templates of the 'Home' page. Clicking on 'Save As' will bring you to the 'Chemistry Search' page. Click on 'Edit' for Sample Source under Search Criteria of the Chemistry Search page in Figure 1a. Select 'Soil' under 'Value' and click 'Update' to accept the changed value in Figure 1b. Clicking on 'Check Search Expression' to ensure that 'Search Expression is valid' in Figure 1c. Click on 'Save Search' to save the search as "A chemistry soil data check". Clicking on 'Show Data' will bring you to the Results page for the searched Chemistry Data.



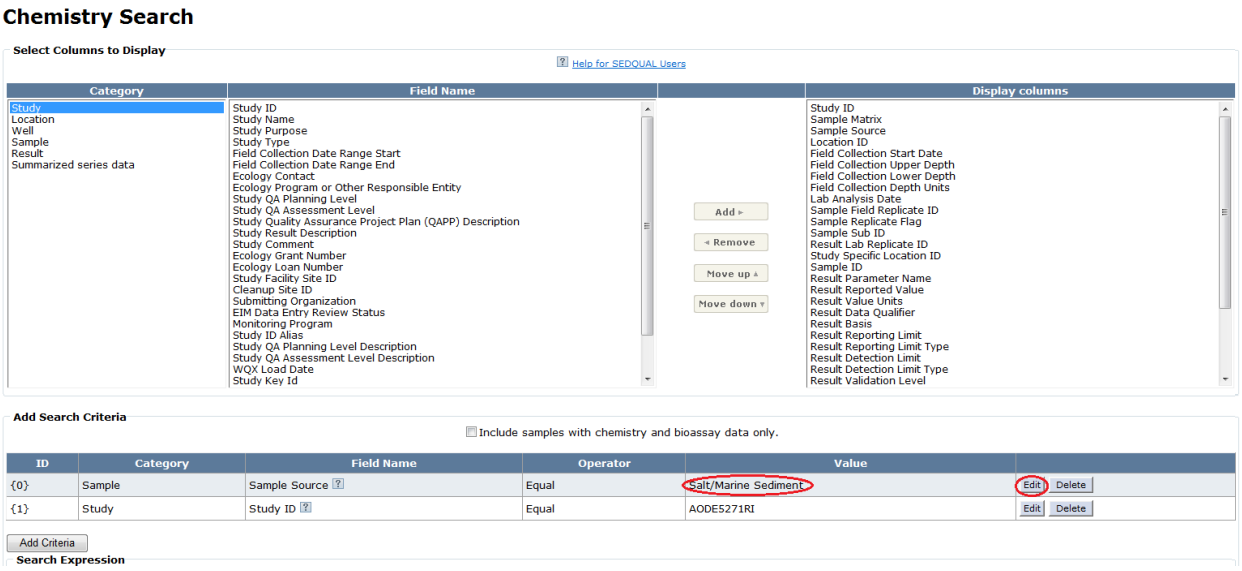


Figure 1a - MyEIM Chemistry Search Page for Sediment Data Search

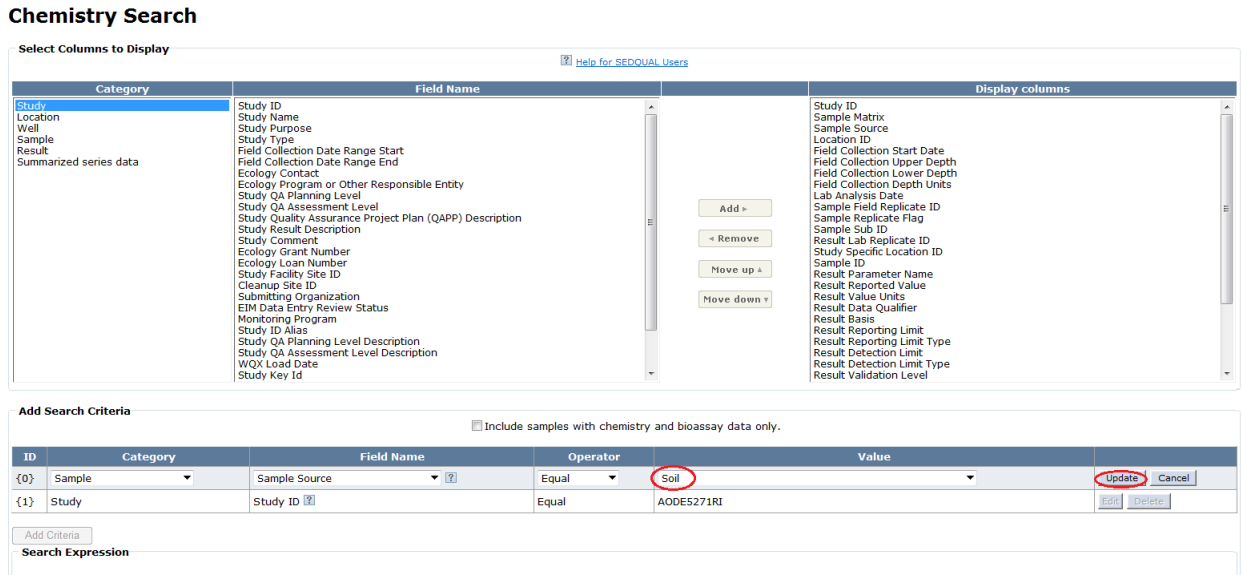


Figure 1b – Changing MyEIM Chemistry Search Page from Sediment to Soil

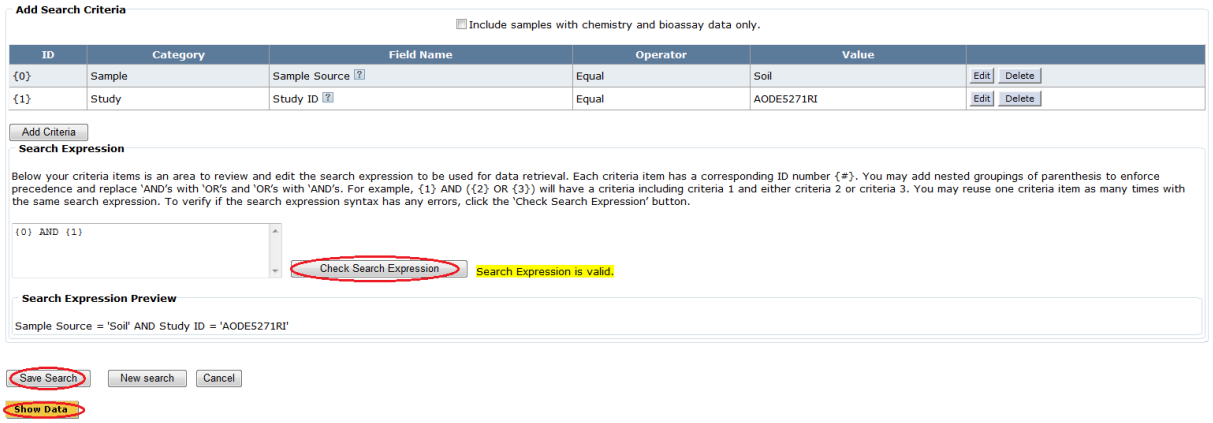


Figure 1c - MyEIM Chemistry Search Page for Soil Data Search

On the searched Results page for Chemistry Data, click the 'Analyze Data' link in the upper left corner of the content page. This link will take you to the "Choose Comparison Criteria" page of the Analysis application.

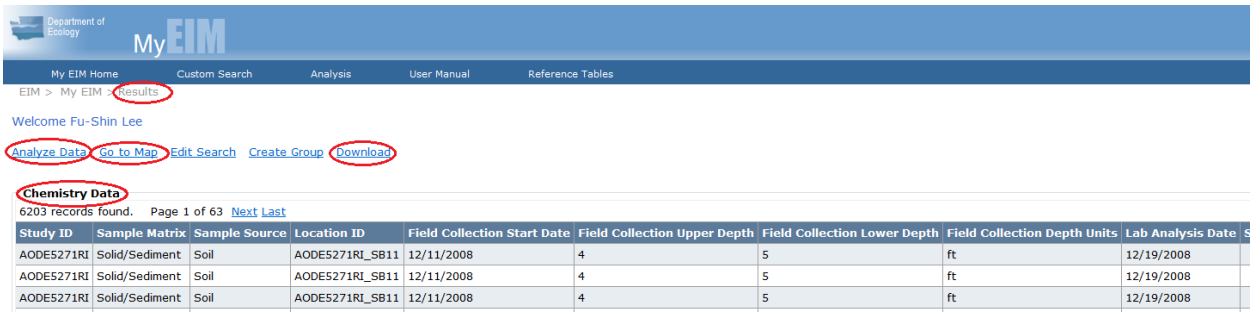


Figure 2 - MyEIM Results Page

Custom Search hands off the results at the back end to Analysis when you come into the Analysis application.

STANDARD ANALYSIS

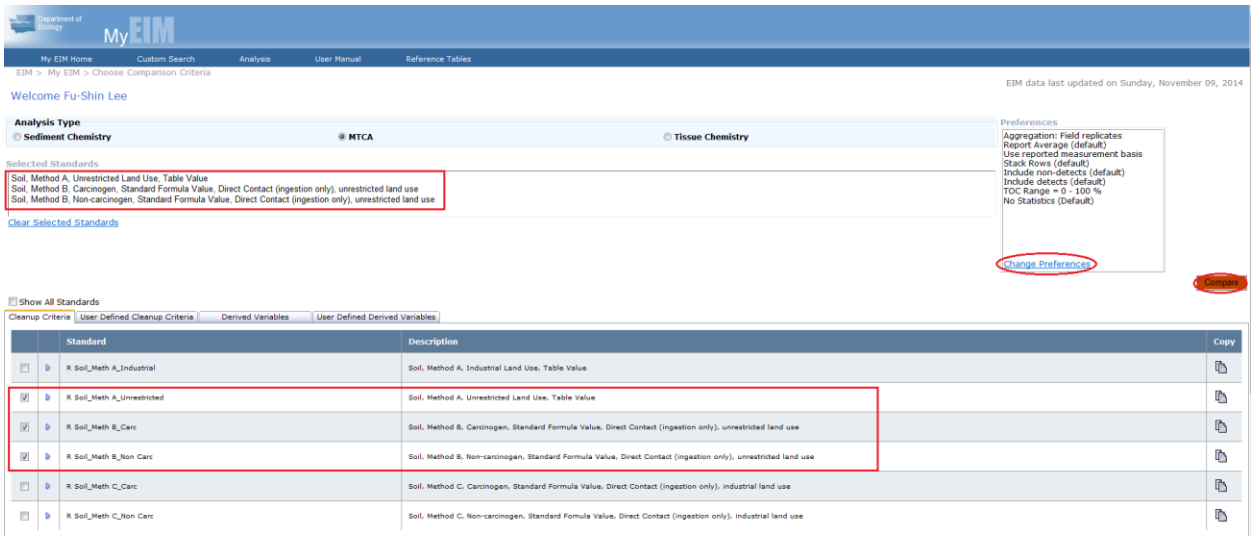
Two following pages for chemistry data analysis will be shown in the order of analysis process:

- Choose Comparison Criteria
- Analysis Results

CHOOSE COMPARISON CRITERIA PAGE

The first step in the Analysis process is to collect settings to conduct analysis on the data received from the Chemistry Search application. The *'Choose Comparison Criteria'* page is the first step in analyzing your data. It is important to note the different elements of this page which consist of the following components:

At the top of the page is the *''Welcome Banner'* displaying user's name and MyEIM navigation menu. Below this banner is the data *'Analysis Type'* (e.g., Sediment Chemistry, MTCA, Tissue Chemistry) and *'Selected Standards'* list box which displays the standards you have selected to compare your searched chemistry data against. To the right of the analysis and selected standards is the *'Selected Preferences'* summary. A prominent '*Compare'* button is just below the Selected Preferences summary detail container. The Show All Standards checkbox sits below the *'Clear Selected Standards*'. The Criteria and Variables grid is the main grid on the page, organized by a set of page tabs, Cleanup Criteria, User Defined Cleanup Criteria, Derived Variables and User Defined Derived Variables, which allows the users to select established and/or user defined cleanup criteria, and to create user defined cleanup criteria and derived variables. Clicking on the blue arrow next to the selected standard or variable will show you the constituents of the selected criteria and variable at the bottom of the page in Figure 3a.



Soil, Method A, Unrestricted Land Use, Table Value

Chemical Name	Concentration	Unit Of Measure	Measurement Basis	Comments
1,1,1-Trichloroethane	2	mg/kg	dry	
4,4'-DDT	3	mg/kg	dry	
arsenic	20	mg/kg	dry	
benzene	0.03	mg/kg	dry	
benzo(a)pyrene	0.1	mg/kg	dry	
cadmium in soil	2	mg/kg	dry	
chromium(III)	2000	mg/kg	dry	
chromium(VI)	19	mg/kg	dry	
Diesel Range Organics	2000	mg/kg	dry	
ethylbenzene	6	mg/kg	dry	

Show page: 1 2 3 (Total Records: 26) Records Per Page: 10

Figure 3a - MyEIM Analysis - Choose Comparison Criteria Page

The options and features in the 'Choose Comparison Criteria' page are detailed below.

Analysis Type

MyEIM supports analysis of sediment data, MTCA data (soil and water), and tissue data. These three types of analyses differ in the data reduction logic and statistical options. MyEIM will identify the most matching analysis type based on the specific sample source of data you search. MTCA was selected in this screen shot, since Soil was selected for Sample Source in MyEIM Chemistry Search page. Users need to decide what type of analysis is appropriate for the data obtained from custom query. MyEIM is currently designed to analyze one sample source of searched data each time.

CLEANUP CRITERIA

Cleanup Criteria is one of four options under the Cleanup Criteria and Derived Variables grid. MyEIM Cleanup criteria have all the MTCA Method A, B and C cleanup criteria for air, groundwater, soil and surface water, CWA 304, NTR and WAC 173-201 surface water criteria, federal and state Maximum Contaminant Level (MCL), and federal Maximum Contaminant

Level Goal (MCLG). MyEIM will display the applicable cleanup criteria per selected specific sample source of searched chemistry data. For example, when soil is selected as the sample source of the searched chemistry data, cleanup criteria will automatically display the MTCA Method A, B and C cleanup criteria for soil. The criteria housed under Cleanup Criteria will be updated, when the regulatory or non-regulatory criteria are updated.

Selected Standards

The Selected Standards box generated will display the list of standards (also called 'comparison criteria') selected to use for chemistry data analysis. Criteria are added or removed from this box by checking or un-checking the rows in the Cleanup Criteria and User Defined Cleanup Criteria grid.

SELECTED PREFERENCES

The Selected Preferences summary displays (figure 3b) analysis and statistical options and 'Statistical Parameters' that will be used during the execution of the analysis. You have access to the 'Analysis Criteria' and 'Statistical Parameters' settings by clicking the "Change Preferences" link at the bottom left corner of the Selected Preferences summary. After you review the review and select your 'Analysis Criteria' and 'Statistical Parameters' settings, in order to return to the Choose Comparison Criteria page, click 'OK' to accept your changes or 'Cancel' button to accept default existing settings.

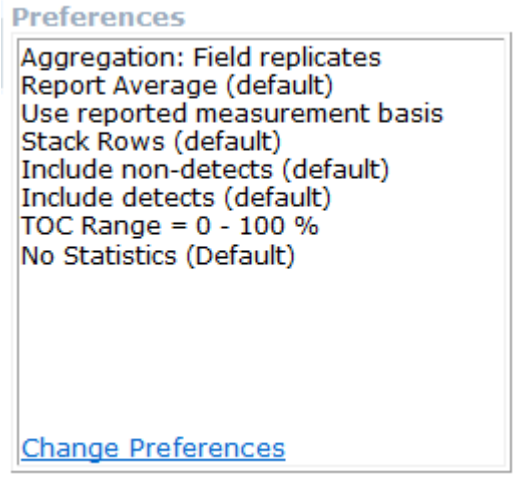


Figure 3b - Default Settings for Soil Chemistry Data Analysis in Preferences Box

The preferences pop up window (Figure 3c) has two major groups of options, Analysis Criteria and Statistical Parameters.

The option groups in 'Analysis Criteria' have settings for how the data will be aggregated for criteria comparison and derived variable calculations, how the data will be compared to the adjusted cleanup criteria using Cleanup Criteria Scaling Factor, as well as output results display options. The options for Analysis Criteria will be detailed under ANALYSIS CRITERIA.

The 'Statistics Parameters' group has settings used exclusively for statistical analysis. The 'Statistics Parameters' group has settings used exclusively for sediment data statistical analysis (Method and lab). However statistical analysis and display depend on all analysis and statistical settings.

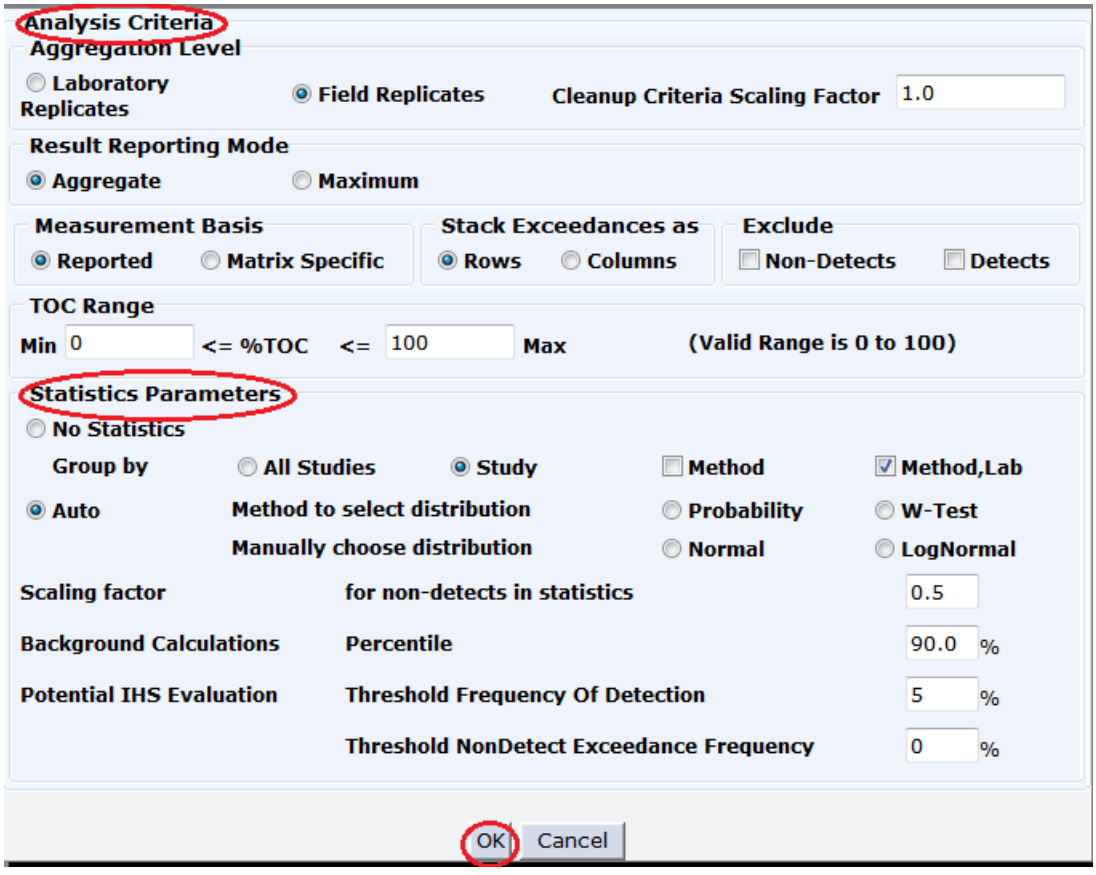


Figure 3c - Change Preferences Dialog for MTCA Chemistry

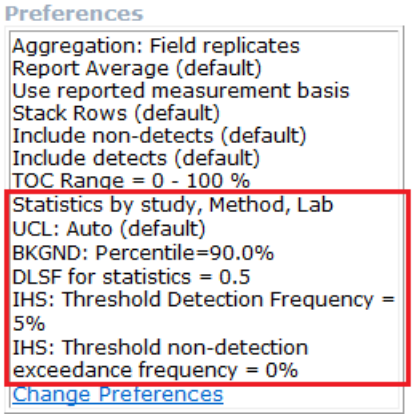


Figure 3d - Selected Statistical Settings in Preferences Box

ANALYSIS CRITERIA

Aggregation Level

The default aggregation level for uplands data analysis is at the field replicate level. If there are laboratory replicates reported, MyEIM carries out data reduction as per the logic described in Appendix E. Data reduction at the field replicates level yields one value between the primary and the field replicate sample results. Field replicates level is chosen by default and always yields one value for each sample. However, lab replicate level aggregation may be chosen when the user needs to view and analyze details of derived variables calculation such as TEQ calculations. Derived variables are calculated for each field replicate and consolidated if more than one field replicate exists to get one value at the field replicate data aggregation level.

Result Reporting Mode

This option sets the rule for data reduction. It provides two options: aggregate rule and maximum rule. Please refer to Appendix E for details on how these rules are implemented.

Measurement Basis

By default, reported measurement basis is used for all calculations. MyEIM will automatically assign dry for soil/sediment sample and wet for water samples. In cases where measurement basis is wrongly reported, MyEIM allows users to override the reported measurement basis with a matrix specific measurement basis. In order to assign an override value automatically where applicable, you will need to select the 'Matrix Specific' option.

Stack Exceedances

"Stacking Exceedances" refers to the display output of the analysis results. The options are to display exceedances in either columns or rows. To demonstrate, let's use an example with two criteria selected.

If "Stack Exceedances" is set to "Columns," then for each row in the data results, there will be one row in the analyzed results. Each of these rows will have full sets of analysis columns, one for each chosen criteria (figure 4a). This option is currently not working, and will be addressed when the end users see the strong needs of using it.

ChemicalName	0_CriteriaName	0_ChemicalConc	0_CriteriaConc	0_CriteriaUOM	0_CriteriaBasis	0_Exceedance	0_HitOrNot	0_Comment	1_CriteriaName	1_ChemicalConc	1_CriteriaConc
dichlorobenzidine;3,3'-									NR Fish_EPA3HHRBC2008_C	0.023	0.007
aluminum	NR Fish_EPA3HHRBC2008_NC	16	1400	mg/kg	wet	0.01215		OK			
antimony	NR Fish_EPA3HHRBC2008_NC	0.05	0.54	mg/kg	wet	0.09242		OK			
arsenic	NR Fish_EPA3HHRBC2008_NC	2.6	0.41	mg/kg	wet	6.502	Hit	OK	NR Fish_EPA3HHRBC2008_C	2.6	0.0021
barium and compounds	NR Fish_EPA3HHRBC2008_NC	0.99	270	mg/kg	wet	0.003674		OK			
beryllium	NR Fish_EPA3HHRBC2008_NC	0.05	2.7	mg/kg	wet	0.01852		OK			
bis(2-ethylhexyl) phthalate	NR Fish_EPA3HHRBC2008_NC	0.1	27	mg/kg	wet	0.003704		OK	NR Fish_EPA3HHRBC2008_C	0.1	0.22
cadmium	NR Fish_EPA3HHRBC2008_NC	0.55	1.4	mg/kg	wet	0.4096		OK			
Cobalt	NR Fish_EPA3HHRBC2008_NC	0.26	0.41	mg/kg	wet	0.6355		OK			

Figure 4a – Analyzed results stacked in columns. Notice the 0_ and 1_ in front of the column names.

If "Rows" is selected, the grid will have multiple analyzed rows for each data result; one for each chosen criteria group (figure 4b).

ChemicalName	CriteriaName	ChemicalConc	CriteriaConc	CriteriaUOM	CriteriaBasis	Exceedance	HitOrNot	Comment
dichlorobenzidine;3,3'-	NR Fish_EPA3HHRBC2008_C	0.023	0.007	mg/kg	wet	3.281	Hit	OK
aluminum	NR Fish_EPA3HHRBC2008_NC	16	1400	mg/kg	wet	0.01215		OK
antimony	NR Fish_EPA3HHRBC2008_NC	0.05	0.54	mg/kg	wet	0.09242		OK
arsenic	NR Fish_EPA3HHRBC2008_NC	2.6	0.41	mg/kg	wet	6.502	Hit	OK
arsenic	NR Fish_EPA3HHRBC2008_C	2.6	0.0021	mg/kg	wet	1257	Hit	OK
barium and compounds	NR Fish_EPA3HHRBC2008_NC	0.99	270	mg/kg	wet	0.003674		OK
beryllium	NR Fish_EPA3HHRBC2008_NC	0.05	2.7	mg/kg	wet	0.01852		OK
bis(2-ethylhexyl)	NR	0.1	27	mg/kg	wet	0.003704		OK

Figure 4b – Analyzed results stacked in rows. Notice Chemical Name is duplicated if in criteria.

Exclude

Check the box next to either Detects or Non-Detects to exclude them from the results output (Selecting both Non-Detects and Detects will forcefully exclude ALL results output).

TOC Range

Set the Total Organic Carbon (TOC) concentration minimum value and maximum value. Query results that have a reported TOC value outside of the range entered here will be excluded from analysis.

Statistics Parameters

MyEIM allows users to compute statistics on data reduced concentrations for every chemical reported in each study through 'Study' or across all studies through 'All Studies' or in combination with Method or Method and Lab. Please refer to the chapter on MTCA Statistics for details. Select All Studies to identify potential indicator hazardous substances, to calculate background and 95% UCL of the mean. Select Study and Method and Lab to analyze and verify the data versus the SAP / QAPP and the data report package

Compare Button

Clicking this button will begin the analysis processing and bring you to the Analysis Results page, when the analysis is completed. All of the settings you have chosen will be sent to MyEIM processors for analysis.

Clear Selected Standards

Clicking this link will unselect both standard and user defined cleanup criteria listed in selected standards list.

Show All Standards Checkbox

By default, this box remains unchecked. In this case, only the criteria that have the same sample matrix and sample source as your search results will appear under the "Standard Cleanup Criteria" tab.

If the "Show All Standards" box is checked, all standard criteria will be displayed, including those that can't be matched to your search results based on sample matrix and sample source.

Note: The analysis processor will compare search results to any standards, even if they are incompatible in terms of sample matrix and sample source. This feature is made available for cross media analysis, however, caution is advised. In either case, the comparison will be made only if measurement basis and unit of measurement are compatible with those of the chosen criteria.

Criteria and Variables Grid

The Criteria and Variables grids display Standard Criteria, User Defined Criteria, Derived Variables and User Defined Derived Variables, and, constituents in each of these four types of criteria items. These four grids are discussed in more detail below.

Constituents List

The Constituents List displays detailed information for the selected standard. This includes chemical name, measurement basis, cleanup concentration, and unit of measure. The list can be exported to Excel for further analysis.

Cleanup Criteria Tab

The simplest analysis that can be performed is to select an existing standard under the Cleanup Criteria tab, and then click the Compare button. The list of constituents associated with each standard can be viewed by clicking the blue arrow located next to the check-box (figure 3a). This list can also be exported to Excel.

User Defined Cleanup Criteria Tab

Users can customize cleanup criteria in the user defined cleanup criteria and use those criteria for comparison. This will be discussed in more detail later in this chapter.

Derived Variables Tab

This tab lists available standard derived variables. There are two types of standard derived variables, Simple Derived Variables and Weighted Derived Variables. Simple derived variables had all constituents equally weighted. In weighted derived variables, constituent weights are fractions. Simple derived variables include Total Benzofluoranthenes (BFA), Polychlorinated Biphenyls (PCBs), Low Molecular Weight Polycyclic Aromatic Hydrocarbons (LPAH), High Molecular Weight Polycyclic Aromatic Hydrocarbons (HPAH), PCB Aroclor Sum, PCB Congener Sum, Total PAHs, Total DDDs, Total DDEs, Total DDTs and Particle/Grain Size, Fines (Silt/Clay). Weighted derived variables include Carcinogenic Polycyclic Aromatic Hydrocarbons as TEQs (cPAH-TEQ), Dioxin/Furan-TEQ, Dioxin-like PCB TEQ and Total 2,3,7,8-TCDD TEQ. Percent Fines and weighted derived variables need to be defined in the user defined cleanup criteria in order to be calculated, compared to the criteria and displayed in the results output

User Defined Derived Variables Tab

Users can customize derived variables under User Defined Derived Variables tab and use them in the User Defined Cleanup Criteria. This feature will be discussed later in this chapter.

EXERCISE 1: COMPARING TO PREDEFINED STANDARDS

(1) On the Home page, select 'Chemistry sediment data check' in Search Templates (Figure 5). Clicking on 'Save As' will bring you to the 'Chemistry Search' page.

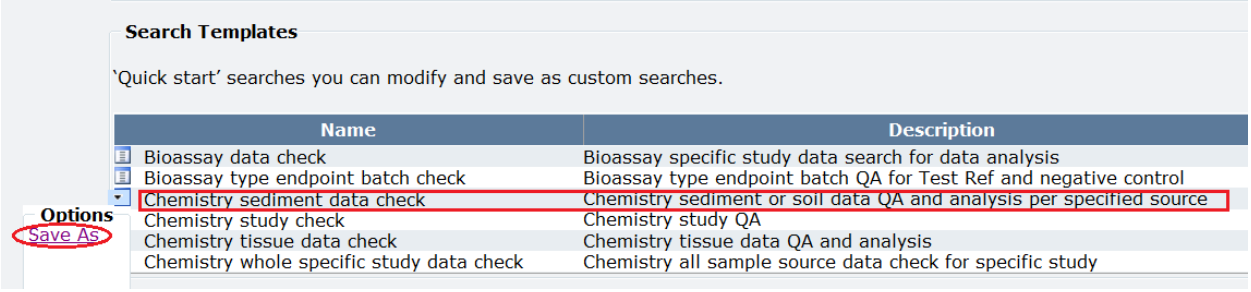


Figure 5 - MyEIM Home Page

(2) On the Chemistry Search page (Figure 6a), click on 'Edit' for Sample Source under Search Criteria. Change 'Value' for Salt/Marine Sediment to Soil, and click 'Update' to accept the changed value (Figure 6b). Clicking on 'Check Search Expression' to ensure that yellow highlighted 'Search Expression is valid' is shown (Figure 6c). Click on 'Save Search'. Type 'A chemistry soil data check' in Search Title box and click on 'Save Search' in Figure 6d to save 'A chemistry soil data check' in your Custom Search. Clicking on 'Show Data' will bring you to the Results page for the searched Chemistry Data (Figure 7).

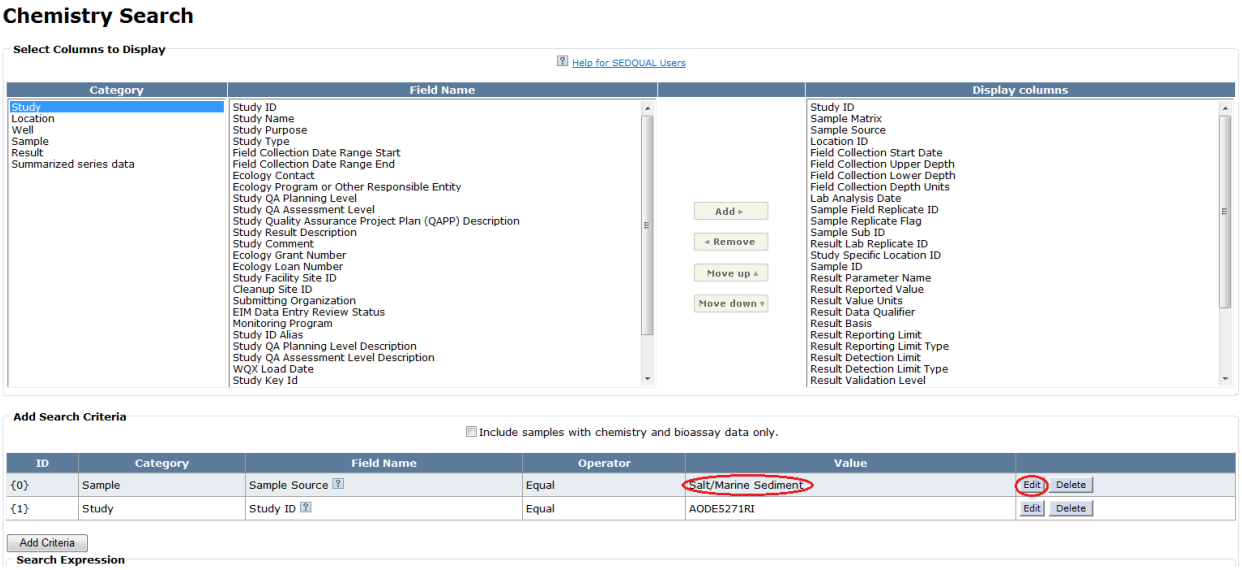


Figure 6a - MyEIM Chemistry Search Page for Sediment Data Search

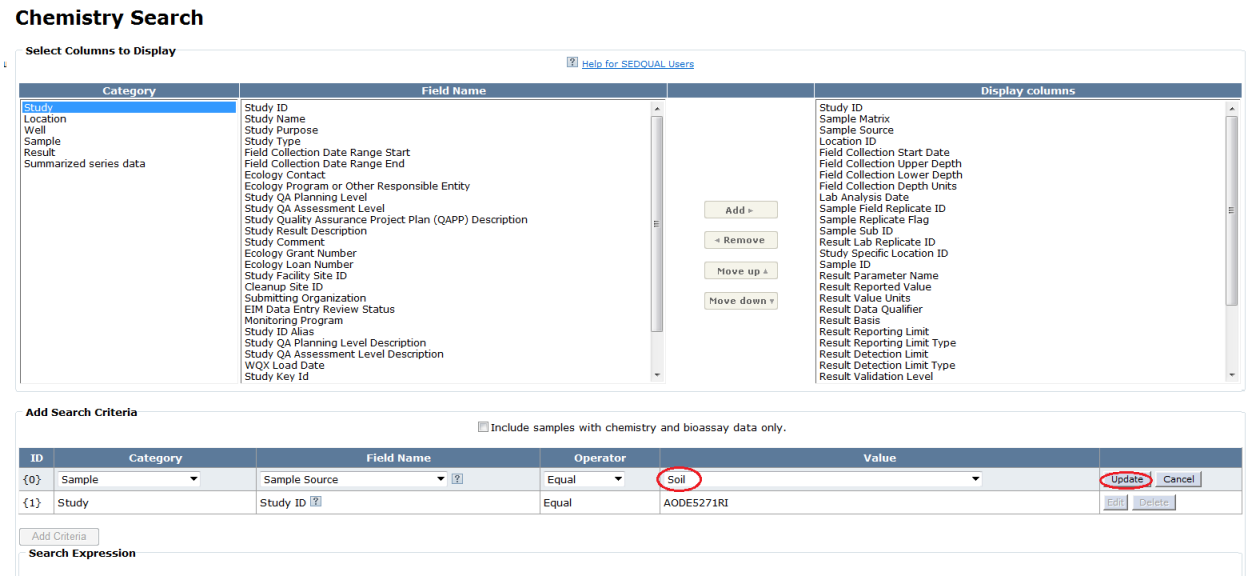


Figure 6b – Changing MyEIM Chemistry Search Page from Sediment to Soil

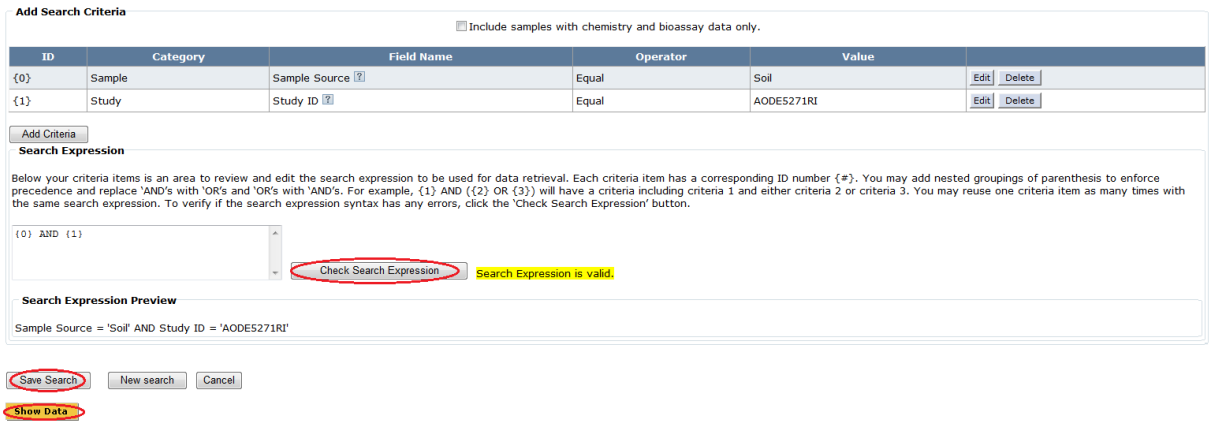


Figure 6c - MyEIM Chemistry Search Page for Soil Data Search

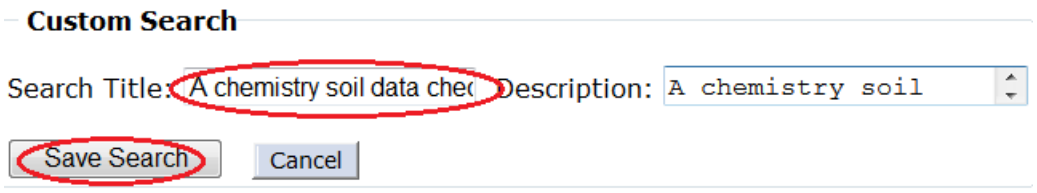


Figure 6d – Save 'A chemistry soil data check'

(3) On the Results page (Figure 7), clicking on 'Analyze Data' will bring you to the 'Choose Comparison Criteria' page.

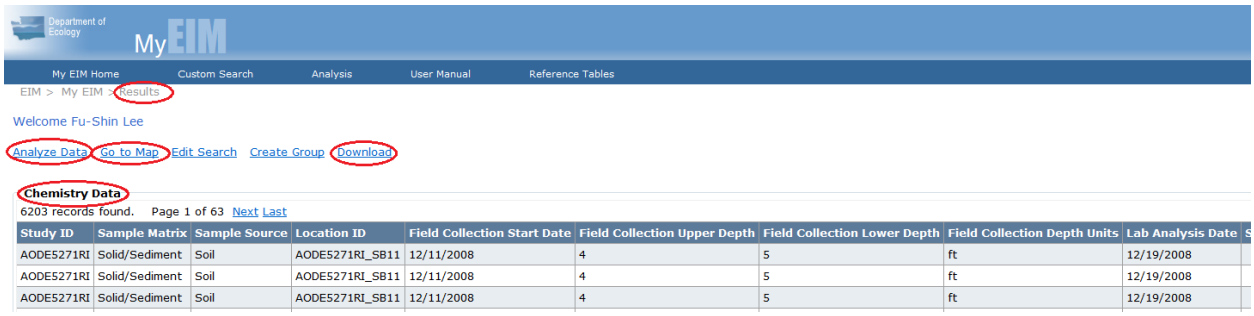


Figure 7 - MyEIM Results Page

(4) On the 'Choose Comparison Criteria' page (Figure 8), clicking the check boxes for R Soil_Meth A_Unrestricted from the standard 'Cleanup Criteria' tab will bring this selected criteria to the Selected Standards box .

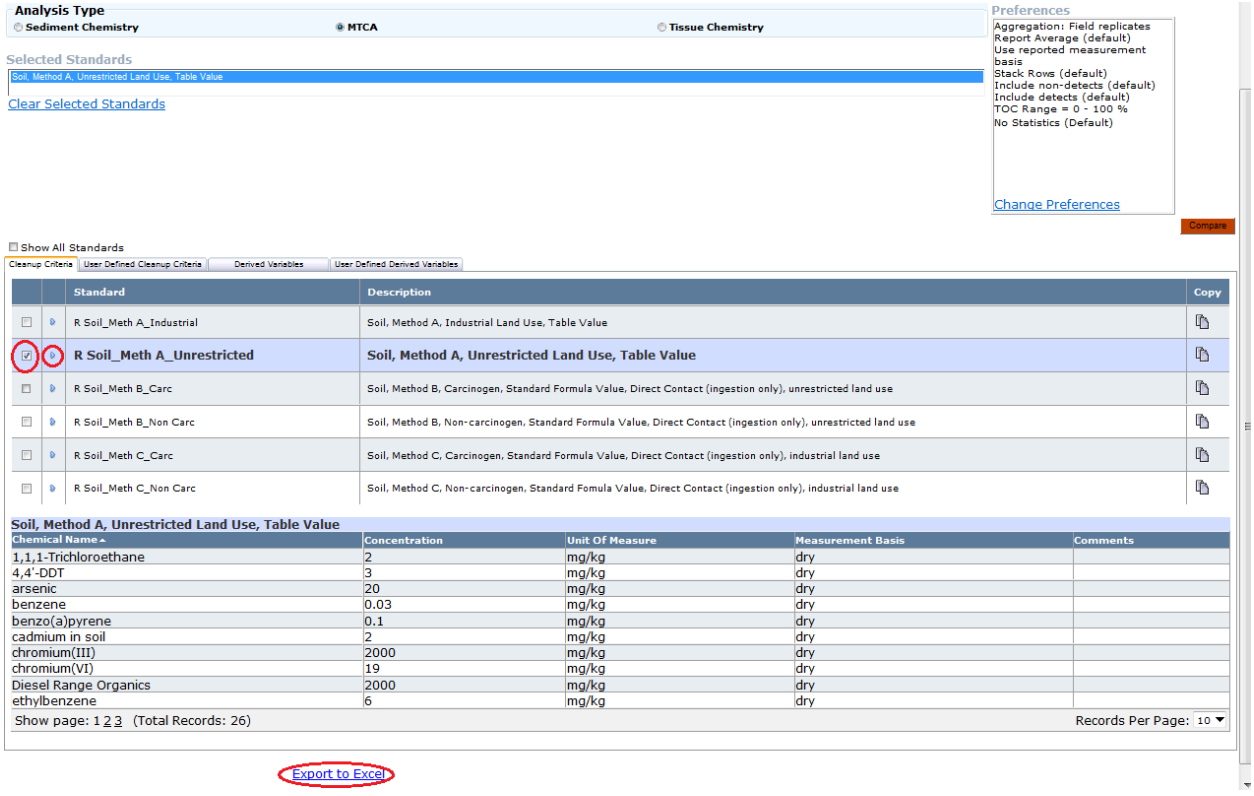


Figure 8 – R Soil_Meth A_Unrestricted *Selected*

Note: Once you select an item from the list, it will be added into the Selected Standards box.

(5) In the preferences, click on Change Preferences to set data aggregation level to Laboratory Replicates, so that you can view derived variables details.

Figure 9 – Set Lab Replicates aggregation level to view derived variable detail.

(6) Click the Compare button. You will be transferred from this page to the Processor page while the analysis is being performed as shown in Figure 9. This page displays the process status, along with the total number of rows received from the database and from analysis.

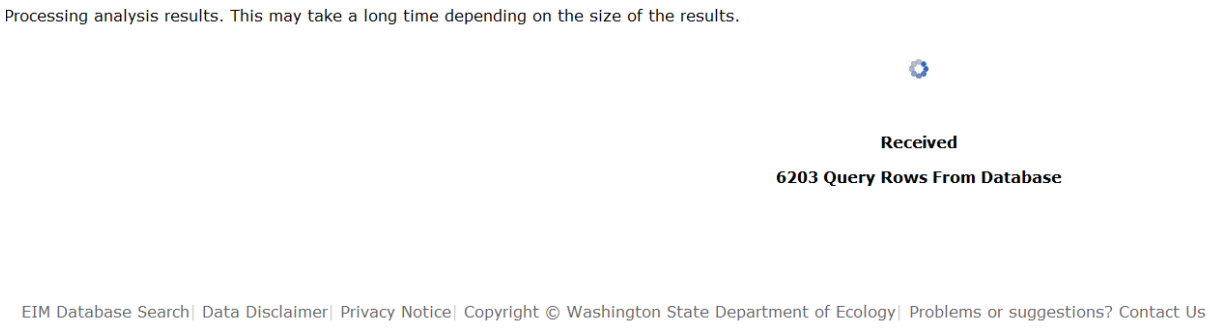


Figure 10 – Analysis processing update real time message

(7) As the database is streaming the data to the chemistry analysis processors, queried and processed results counts (Figure 10) will be displayed. When analysis processing is complete, the Analysis Results page (Figure 11) will show the chemistry comparison results and derived variables of your analysis.

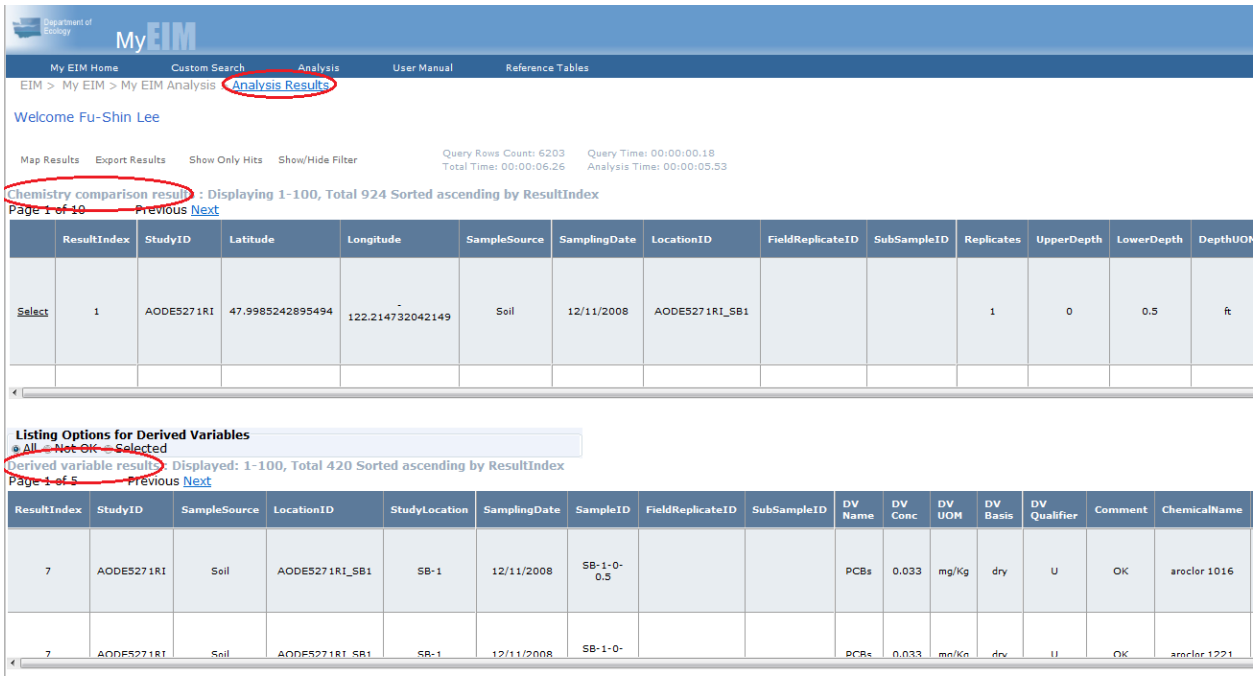


Figure 11- Analysis Results page

That's it! With just a few clicks you have taken a result set and compared it to standard criteria. The analysis results are laid out in two grids. The top grid is the Chemistry Analysis: Comparison Results grid. Below this grid derived variables calculation details is displayed.

Note: A derived variable calculation is performed only when a selected standard has derived variables listed for comparison. Field replicate aggregated results will not display derived variable calculation results. The derived variables details are displayed and downloadable when the data are aggregated at laboratory replicates level and a selected standard has derived variables listed for comparison.

ANALYSIS RESULTS PAGE

Results are displayed on the screen through the Analysis Results page. From here you can map the analyzed results through 'Map Results', filter the results down to a smaller subset of the full analyzed dataset through 'Show/Hide Filter' or 'Show Only Hits', or export the results to a spreadsheet file through 'Export Results' and 'Export Statistics' when analyzed and available. These key functions, 'Map Results', 'Show/Hide Filter', 'Show Only Hits', 'Export Results' and 'Export Statistics', will be detailed in the exercises.

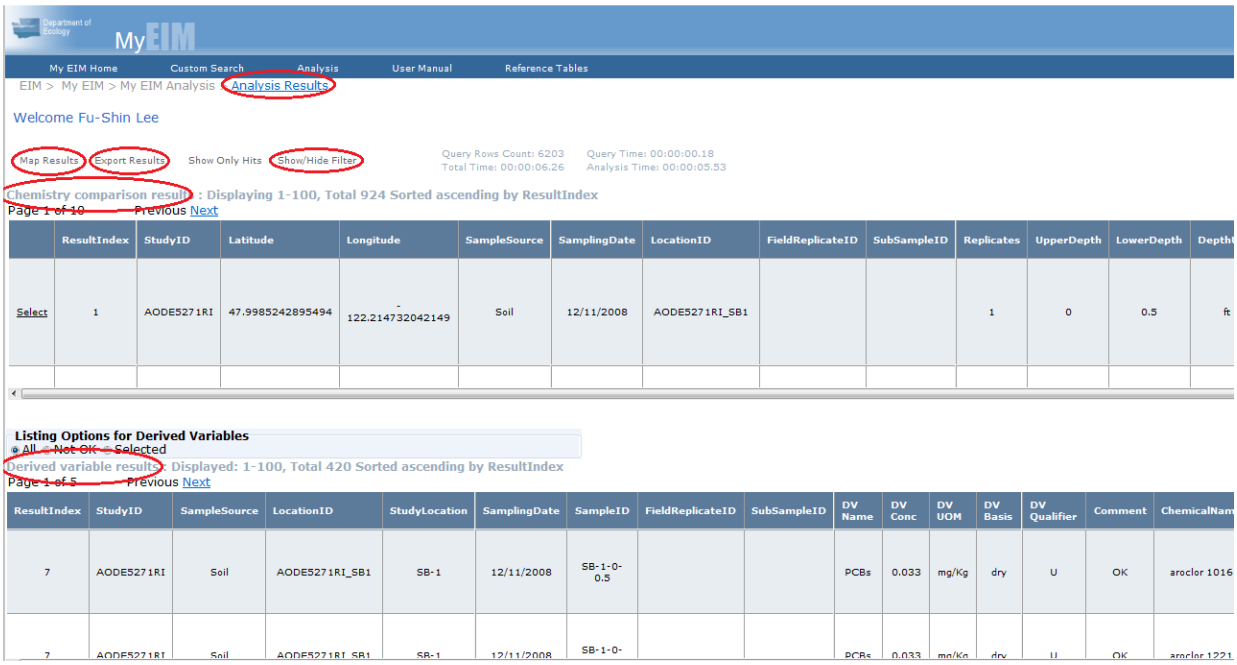


Figure 11a - Display Results page contains two grids: criteria comparison and derived variables.

The Analysis Results page contains two or three grids, depending on whether the statistical parameters are selected.

- Chemistry comparison results
- Derived variable results
- Statistics variable results

Each grid on this page provides paging through the data 100 rows at a time. This is done by clicking the Previous and Next buttons on the top of the grid. The total number of rows is displayed in the grid title.

COMPARISON RESULT GRID COLUMNS

The upper grid contains the criteria comparison results. A brief explanation of the logic used follows. Please refer to the appropriate appendices for more detail.

- Chemical concentrations at the chosen replicate level are aggregated using the data reduction logic explained in Appendix F, then normalized with respect to the unit of measure and measurement basis of the cleanup criteria before calculating the ratio (chemical concentration divided by criteria concentration) of concentration values to find the Exceedance value.
- Some of the parameters in the cleanup criteria are derived variables. Simple derived variables are calculated using the logic described in Appendix F.
- TEQ weighted derived variables are calculated using the logic described in Appendix G.
- Calculated values of derived variables are used for comparing to criteria values when possible. If a derived variable calculation is not possible for any reason, and reported values of derived variable reported values are available in query data, MyEIM uses reported values for comparison.

Columns of the comparison grid are shown in Figure 11b. The first column has all cells labeled "select". This provides the link between the two grids. If the row contains a derived variable, clicking "select" on this row will filter the details of the derived variable and show it in the second grid. If the row is not a derived variable, then a message will display indicating this row is not a derived variable. Result Index column shows a unique identifier assigned for that row. This identifier is used to link this row to a derived variable detailed in the lower grid. By default, this grid is sorted by the Result Index column. You can change the sort order by clicking on the column header (e.g., click on 'ChemicalName' to resort the grid by the chemical name). All the other columns are reported values obtained from your custom search that identify field replicates.

	ResultIndex	StudyID	Latitude	Longitude	SampleSource	SamplingDate	LocationID	FieldReplicateID	SubSampleID	Replicates	UpperDepth	LowerDepth	DepthUOM
Select	1	AODE5271RI	47.9985242895494	-122.214732042149	Soil	12/11/2008	AODE5271RI_SB1			1	0	0.5	ft
Select	7	AODE5271RI	47.9985242895494	-122.214732042149	Soil	12/11/2008	AODE5271RI_SB1			1	0	0.5	ft

Listing Options for Derived Variables

All Not OK Selected

Derived variable results : Displayed: 1-100, Total 420 Sorted ascending by ResultIndex

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ResultIndex	StudyID	SampleSource	LocationID	StudyLocation	SamplingDate	SampleID	FieldReplicateID	SubSampleID	DV Name	DV Conc	DV UOM	DV Basis	DV Qualifier	Comment	ChemicalName
7	AODE5271RI	Soil	AODE5271RI_SB1	SB-1	12/11/2008	SB-1-0-0.5			PCBs	0.033	mg/Kg	dry	U	OK	aroclor 1016

Figure 11b – Left comparison results grid with lab replicate level data reduction.

StudyLocation	SampleID	ChemicalName	CASNumber	CriteriaName	ChemicalConc	CriteriaConc	CriteriaUOM	CriteriaBasis	Exceedance	HitOrNot	Comment	Qualifier	TOC
SB-1	SB-1-0-0.5	arsenic	7440-38-2	R Soil_Meth A_Unrestricted	6	20	mg/kg	dry	0.3		OK		

Figure 11c – Middle Criteria comparison columns of the comparison results grid.

Note the SampleID column for analysis at the lab replicate level. In some cases, field replicates of the same sample are assigned different SampleIDs. During data reduction at field replicate level of those samples, SampleIDs of field replicates are concatenated.

Figure 11c shows Chemical Name and eight columns specific to each criteria comparison, in addition to *Qualifier* and *Replicates* columns evaluated from data reduction, as well as related reported values of concentration, unit of measure, and measurement basis for each chemical.

The *Chemical Conc* column shows concentration value after normalizing with respect to measurement basis and unit of measure of the criteria.

Criteria Name, Criteria Value, Criteria UOM, and *Criteria Basis* column values are imported from chosen criteria for chemicals in each row.

Exceedance is the ratio of Chemical Conc to Criteria Value.

The *HitOrNot* column indicates if Chemical Conc is greater than the Criteria Value.

The *Comment* column displays a message giving an explanation in case the calculation is unsuccessful, or any non-default feature is used. In case this is a derived variable, the details of the derived variable calculation are also imported here.

The *Qualifier* column displays the qualifier code assigned to the chemical concentration after data reduction.

The *Replicates* column (Figure 11b) shows the number of replicates used in the process of data reduction.

The *TOC* column shows an average of all % TOC values reported under lab or field replicate data aggregation or individually reported % TOC if the sample has no lab or/and field replicates . For TOC value to be displayed it is important to ensure the TOC data is queried as a part of the search data.

ReportedConc	ReportedUOM	ReportedBasis	ReportingLimit	RLType	DetectionLimit	DLType	ReportedComment	AnalysisMethod	AnalysisLab	ValidationLevel	GeoLocation	QAPlanning	Assessment	Contact	Program	Location Setting	Study Type	StudyName
6	mg/Kg	dry	6	MRL	0.58	MDL	OE07F	SW6010B	Analytical Resources Inc (ARI), Seattle WA		71558817	4	4	Park, Hun Seak	ECY-TCP-HQ	LAND	SiteInvestigation	Remedial Investigation Everett Shipyard Property soil, groundwater and sediment.
																		Remedial

Figure 11d – Right Criteria comparison columns of the comparison results grid.

The *Reported Conc* column shows data reduced concentration value based on the data reduction rule chosen in preferences.

The *Reported UOM* column shows unit of measure associated with data reduced concentration.

The *Reported Basis* column shows reported basis for the chemical in the sample.

In case of no data reduction, the *Reported Conc*, *Reported UOM* , and *Reported Basis* columns show reported values from search data. Reporting Limit, RL Type, Detection Limit, and DL show reported values for Result Reporting Limit, Result Reporting Limit Type, Result Detection Limit, and Result Detection Limit Type from the EIM data search.

Analysis Method, Analysis Lab, and Validation Level show reported values for Result Method, Result Lab Name, and Result Validation Level from the EIM data search.

QA Planning, Assessment, Contact, Program, Location Setting, Study Type, and Study Name show reported values for Study QA Planning Level, Study QA Assessment Level, Ecology Contact, Ecology Program or Other Responsible Entity, Location Setting, Study Type, and Study Name from the EIM data search.

DERIVED VARIABLE GRID COLUMNS

The Derived Variable grid is displayed only when data reduction at laboratory level is chosen. The columns, as shown in Figure 12a, are reported values obtained from your custom search that identify field replicates.

Note: All uplands data analysis will need to be carried out at Field Replicate Levels when performing analysis outside of training. For illustration only, data aggregation level at laboratory replicates is deliberately selected in order to demonstrate a derived variable calculation.

ResultIndex	StudyID	SampleSource	LocationID	StudyLocation	SamplingDate	SampleID	FieldReplicateID	SubSampleID
7	AODE5271RI	Soil	AODE5271RI_SB1	SB-1	12/11/2008	SB-1-0-0.5		
7	AODE5271RI	Soil	AODE5271RI_SB1	SB-1	12/11/2008	SB-1-0-		

Figure 12a –Left most columns of the Derived Variable grid.

DV Name	DV Conc	DV UOM	DV Basis	DV Qualifier	Comment	ChemicalName	WeightedConc	% Contribution	TOC	DLSF	Weight
PCBs	0.033	mg/Kg	dry	U	OK	aroclor 1016	0.033	100	2.05		1
PCBs	0.033	mg/Kg	dry	U	OK	aroclor 1221	0.033	100	2.05		1
PCBs	0.033	mg/Kg	dry	U	OK	aroclor 1232	0.033	100	2.05		1
PCBs	0.033	mg/Kg	dry	U	OK	aroclor 1242	0.033	100	2.05		1
PCBs	0.033	mg/Kg	dry	U	OK	aroclor 1248	0.033	100	2.05		1
PCBs	0.033	mg/Kg	dry	U	OK	aroclor 1254	0.033	100	2.05		1
PCBs	0.033	mg/Kg	dry	U	OK	aroclor 1260	0.033	100	2.05		1
PCBs	0.033	mg/Kg	dry	U	OK	aroclor 1016	0.033	100	1.79		1
PCBs	0.033	mg/Kg	dry	U	OK	aroclor 1221	0.033	100	1.79		1
PCBs	0.033	mg/Kg	dry	U	OK	aroclor 1232	0.033	100	1.79		1
PCBs	0.033	mg/Kg	dry	U	OK	aroclor 1242	0.033	100	1.79		1
PCBs	0.033	mg/Kg	dry	U	OK	aroclor 1248	0.033	100	1.79		1
PCBs	0.033	mg/Kg	dry	U	OK	aroclor 1254	0.033	100	1.79		1
PCBs	0.033	mg/Kg	dry	U	OK	aroclor 1260	0.033	100	1.79		1

Figure 12b –Columns specific to calculation details of the Derived Variable.

Columns named *DV Name*, *DV UOM* and *DV basis* show the information from the criteria based on which derived variables are calculated.

Calculated concentration is shown in *DV Conc* column.

The *DV qualifier* shows the code assigned to the calculated value based on the derived variable calculation logic. Derived variable calculation logic please is contained in appendices F and G.

The *Comment* column indicates messages arising from calculation. 'OK' indicates the calculation is completed successfully, and no missing constituents.

For every derived variable there are as many rows as its constituent chemicals, one for each chemical. *Chemical Name* column indicates the name of the constituent.

Weighted Conc shows the concentration of the chemical after normalizing with respect to unit of measure and measurement basis if necessary, and scaled by detection limit scaling factor (DLSF) if concentration is U (non-detect) qualified and scaled by weights as assigned in the definition of the derived variable in the criteria.

The *%Contribution* column shows the contribution of this weighted concentration to the total sum that makes up derived variable concentration.

TOC is the average percent TOC value of the sample at laboratory replicate data aggregation level or the reported TOC value without laboratory/field replicates. For TOC normalization, it is important to ensure the TOC data is queried as a part of the search data.

Detection Limit Scaling Factor (*DLSF*) and **Weight** for each chemical originate from the definition of the derived variable in the criteria.

ReportedConc	ReportedUOM	ReportedBasis	Reported Qualifier	ReportingLimit	RLType	DetectionLimit	DLType	ReportedComment	ValidationLevel	AnalysisMethod	AnalysisLab
33	ug/Kg	dry	U	33	MRL	3.3	MDL	OE07F		SW8082	Analytical Resources Inc (ARI), Seattle WA
33	ug/Kg	dry	U	33	MRL	3.3	MDL	OE07F		SW8082	Analytical Resources Inc

Figure 12c – Columns specific to reported values of the chemical and sample.

UpperDepth	LowerDepth	DepthUOM	Latitude	Longitude	GeoLocation	Study Type	Location Setting	QAPlanning	Assessment	Contact	Program	StudyName
0	0.5	ft	47.9985242895494	-122.214732042149	71558817	SiteInvestigation	LAND	4	4	Park, Hun Seak	ECY-TCP-HQ	Remedial Investigation Everett Shipyard Property soil, groundwater and sediment.
0	0.5	ft	47.9985242895494	-	71558817	SiteInvestigation	LAND	4	4	Park, Hun	ECY-	Remedial Investigation Everett Shipyard

Figure 12d – Right most columns of the Derived Variable grid.

Figure 12c shows the columns specific to the reported values of the chemical and sample from chemistry data search.

Reported Conc shows the data reduced value of the chemical concentration, if the laboratory or field replicate results are reported. Otherwise Reported Conc originate from search results.

Reported UOM and *Reported basis* originate from search results.

Reported Qualifier is the qualifier code arising from data reduction logic or from reported values.

Figure 12d shows the remaining columns of the derived variables grid.

Three *depth* columns are related to the sample identity and the Lat/Long, GeoLocation, and Location Setting column values identify the location.

QA Planning, Assessment, Contact, Program, and Study Name show reported values for Study QA Planning Level, Study QA Assessment Level, Ecology Contact, Ecology Program or Other Responsible Entity, and Study Name from the search results.

In cases where derived variables are calculated, the details of individual chemical constituents (from the top list) are listed in the lower grid. For example, if a criteria constituent of PCB is analyzed against a result containing PCB, the upper grid will display the summary of the evaluated concentration. The lower grid will contain 7 rows of data related to the result row in the upper grid because the PCB derived variable is defined with 7 constituents.

Figure 13 - Filtering of Derived Variables

Filtering of the Derived Variable grid is possible in three ways. These options are available between the upper and lower grids in the Listing Options for Derived Variables.

1. Selecting '*All*' displays all derived variable results.
2. '*Not OK'* only displays those derived variable values where the evaluation of the constituents could not be performed as desired. This is reflected in the comments.
3. The final option is '*Selected'*. It displays only those derived variables that match the selected row in the upper grid. The first column in the upper grid provides the link to display details of a derived variable in the lower grid.

Note: Derived variables are calculated only when defined in selected criteria. Derived variable calculation details are shown only when derived variables are calculated and the data are aggregated at laboratory replicate level. At field replicate level aggregation, the *Derived Variables* grid will be empty, since derived variables are already calculated at lab replicate level and are only data reduced.

EXERCISE 2: MAP RESULTS

The analyzed results can be mapped to show where chemical concentrations exceeded the selected Comparison Criteria. This is done by clicking the Map Results link.

(1) Click on "Map Results".

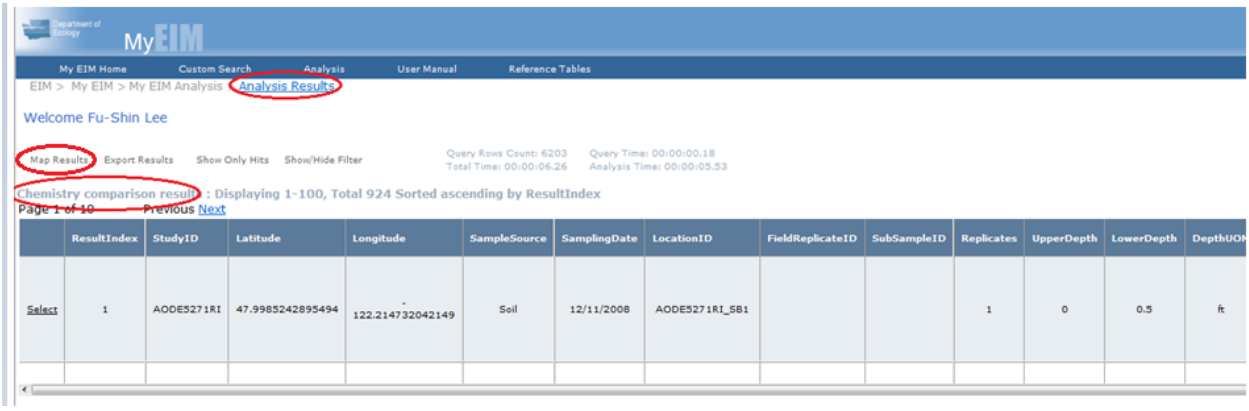

Figure 14 –Map Results link

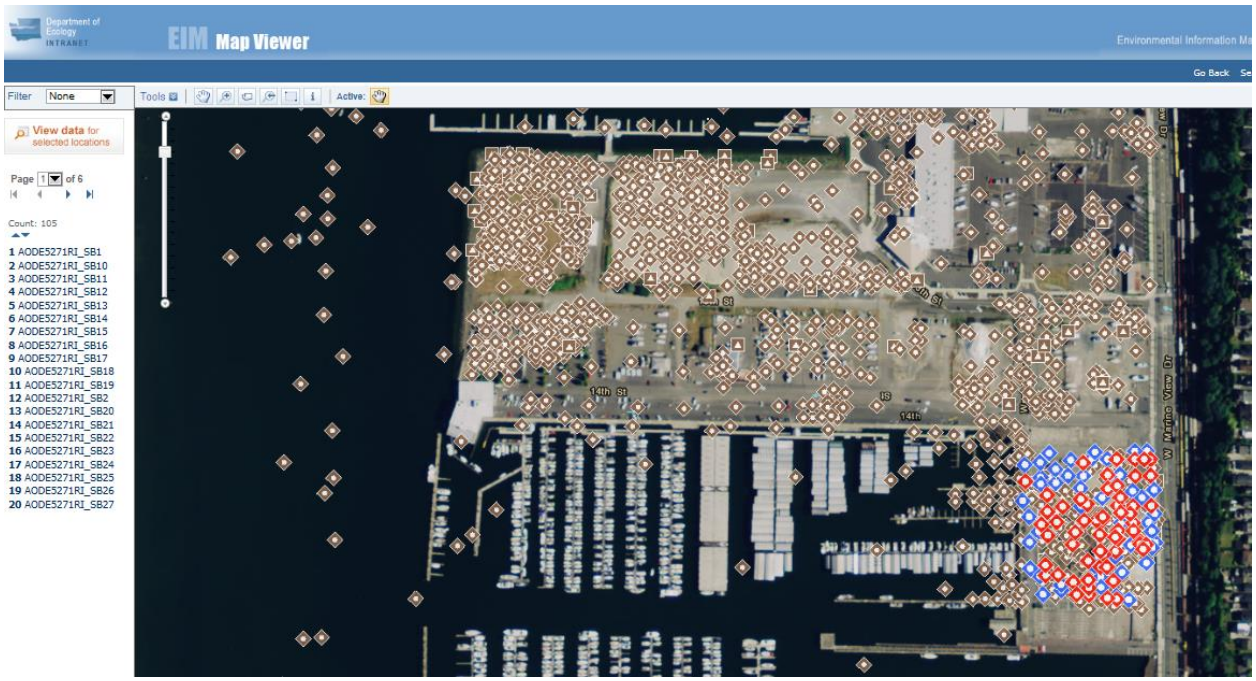

Figure 15 - Mapped analysis results for uplands samples.

When results are mapped, the concentration values for samples exceeding the concentration value of a selected standard result in a dot on the map which is automatically highlighted in Red.

EXERCISE 3: EXPORT RESULTS

Selecting the Export Results link will allow you to download the analyzed results as a CSV file. This file can then be opened in a spreadsheet program such as Microsoft Excel.

(1) Click on the Export Results link on the Analysis Results page.

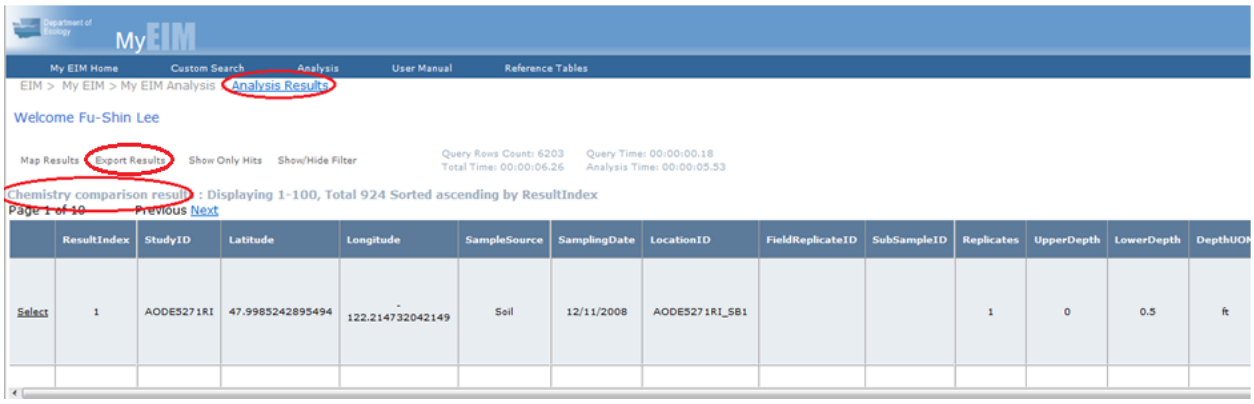

Figure 16 - Export Results link

A dialog box prompt will confirm the file download. Click Open in Figure 17 to bring you to the zip file in Figure 18. This zip file will contain two spreadsheet files, chemistry comparison results at the top grid and derived variable results at the middle grid on Analysis Results page. You can double click on the files to view and save these spreadsheets in your folder.

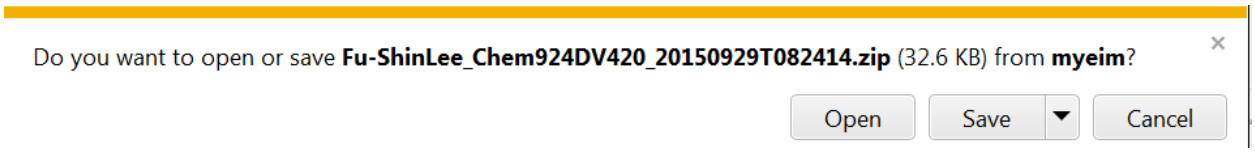

Figure 17 - Export results dialog box.

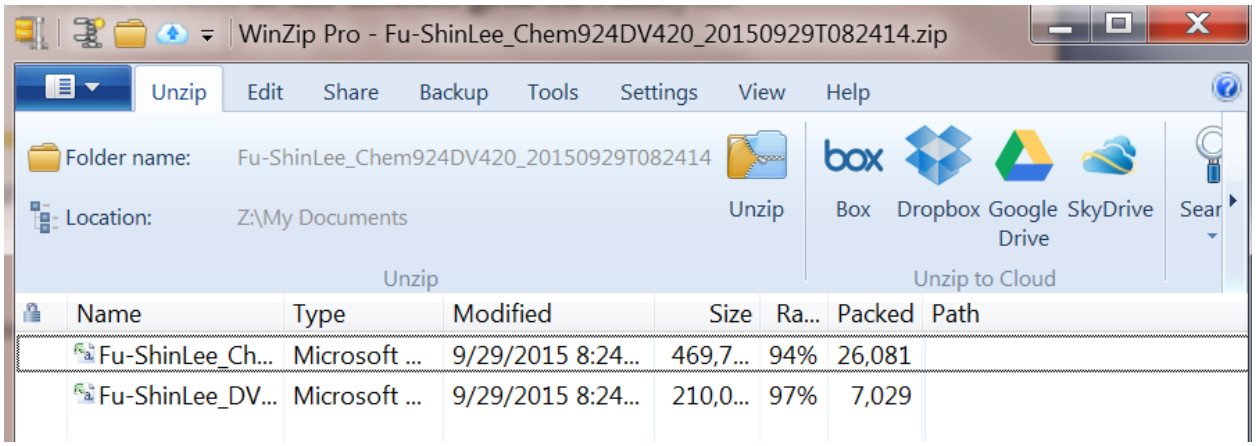

Figure 18 - Export results in Zip File.

EXERCISE 4: SHOW ONLY HITS

The Show Only Hits link will filter the Comparison Results grid to show only those chemicals that exceed the selected standards.

(1) Click on the Show Only Hits link.

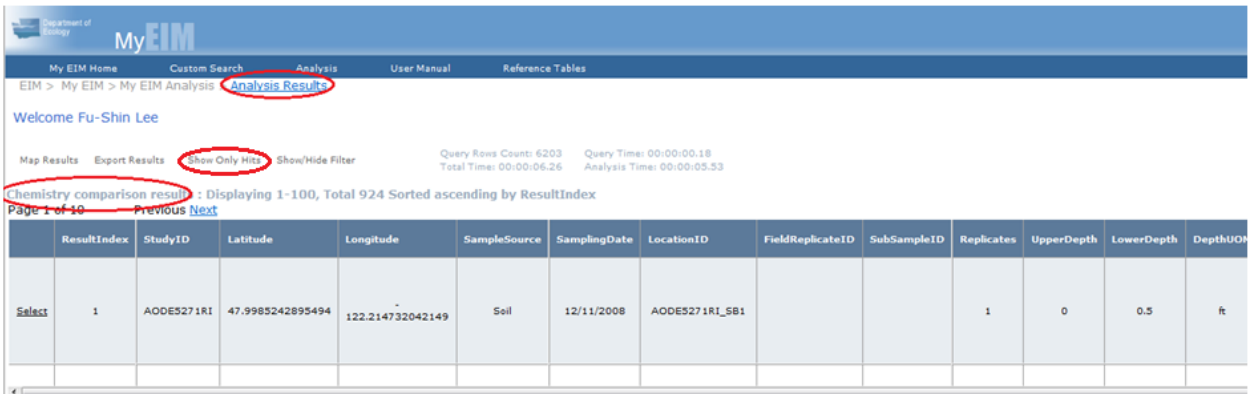

Figure 19 - Show Only Hits link

(2) Notice that only the chemicals exceeding the standard criteria cleanup levels are displayed.

StudyLocation	SampleIDs	ChemicalName	CASNumber	CriteriaName	ChemicalConc	CriteriaConc	CriteriaUOM	CriteriaBasis	Exceedance	HitOrNot	Comment	Qualifier
SB-10	SB-10-0-0.5	arsenic	7440-38-2	R Soil_Meth A_Unrestricted	200	20	mg/kg	dry	10	Hit	OK	
SB-10	SB-10-0-0.5	benzo(a)pyrene	50-32-8	R Soil_Meth A_Unrestricted	0.15	0.1	mg/kg	dry	1.5	Hit	OK	
SB-10	SB-10-0-0.5	lead	7439-92-1	R Soil_Meth A_Unrestricted	290	250	mg/kg	dry	1.176	Hit	OK	

Figure 19 - Result data exceeding the standard.

EXERCISE 5: SHOW/HIDE FILTER

Selecting the Show/Hide Filter link will allow you to place filtering constraints on the analyzed data you are viewing. The previous exercise processed a predefined filter to look for hits.

(1) Click on the Show/Hide Filter link.

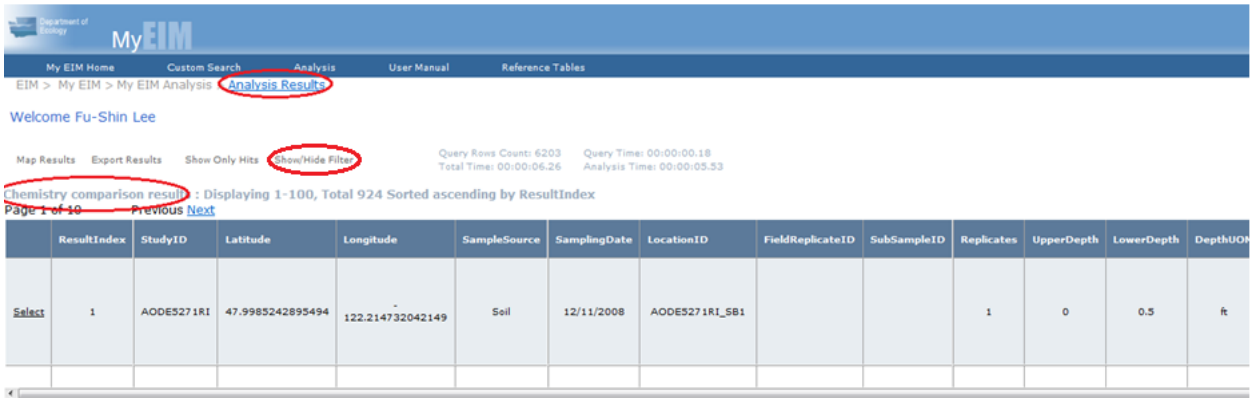

Figure 20 - Show/Hide filter link

(2) The filter appears. The Filter control allows you to filter to a subset of results in the grid.

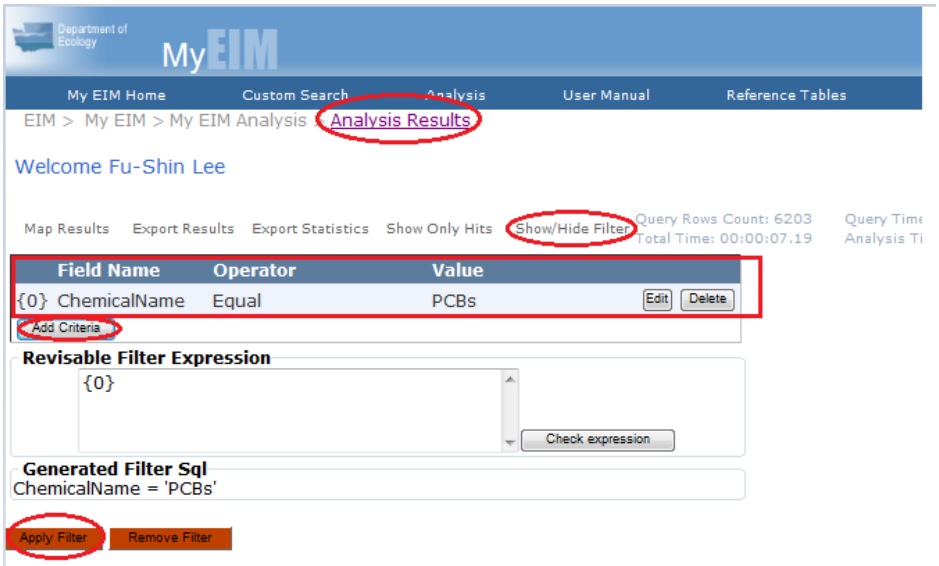

Figure 21 - Show/Hide Filter on Analysis Results Page.

The filter control works just like the Custom Search filter control. To begin, click on the Add Criteria button. A new filter row is displayed.

(3) Select the column name 'Chemical Name' to filter in the "Field Name" dropdown list.

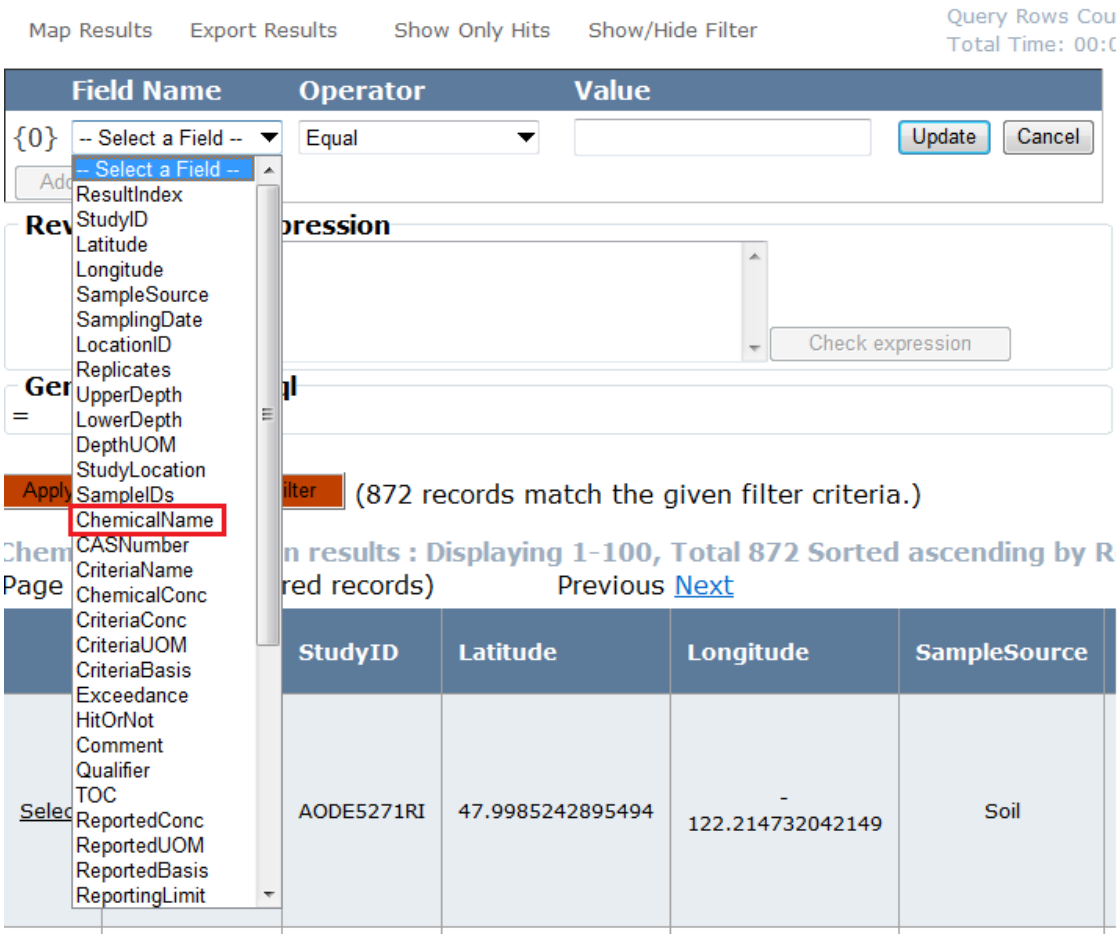

Figure 22 – The Custom Filter Control

(4) Next select the operator. (equal in this example)

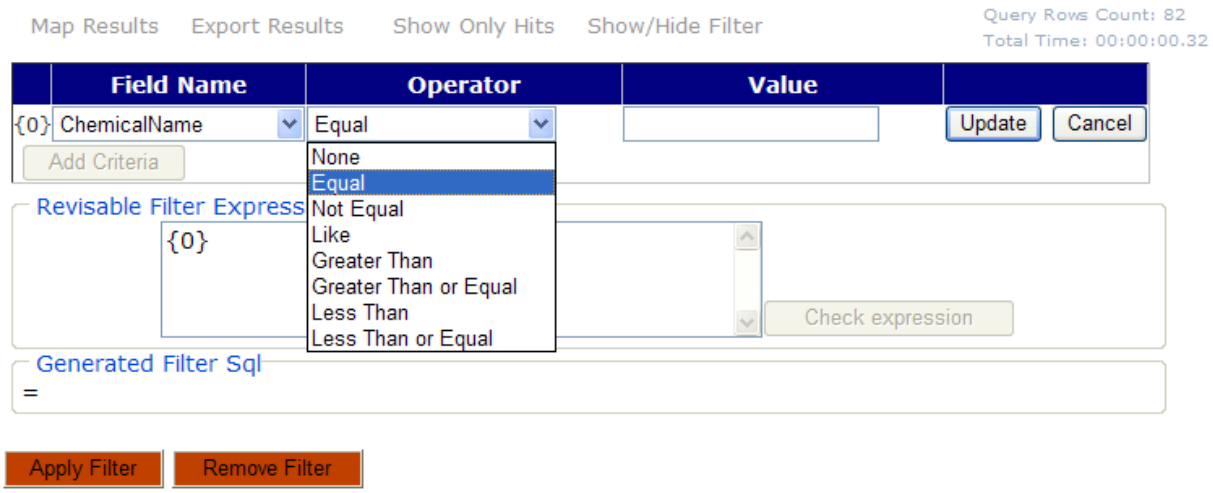

Figure 23 – The Custom Filter Control: select an operator and input a value.

(5) Finally, enter the value for the filter and click the Update button. As you type, distinct values from the columns appear as available values. The response of this drop down list depends on the size of the grid.

(6) Click the Apply Filter button to limit displayed results to those that match the filter.

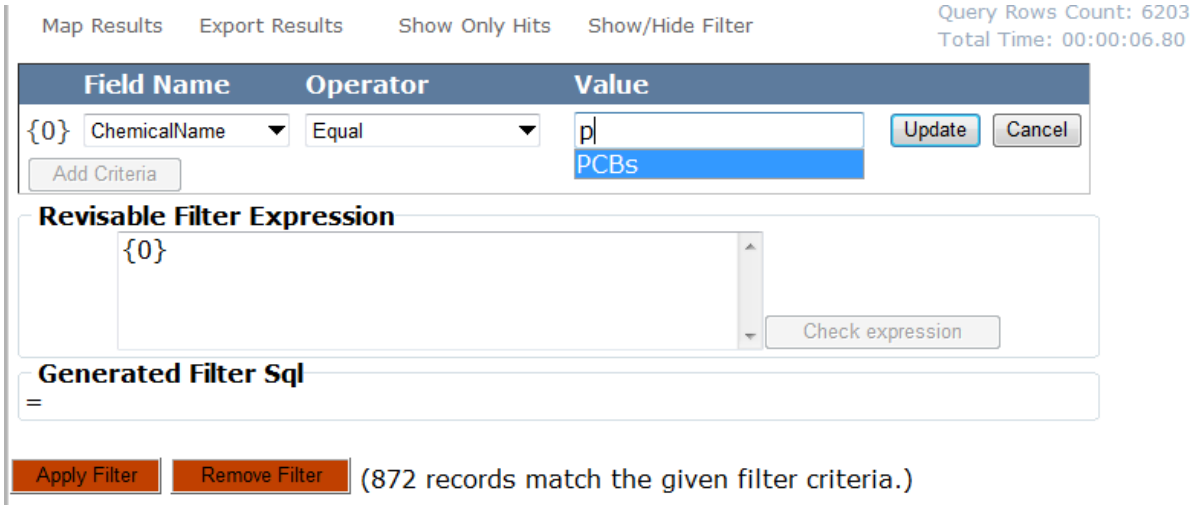

Figure 24 –Filtered to show chemical name = 'PCBs'

(7) Filtered grid appears.

Figure 25 –Filtered to show only records with chemical name of 'PCBs'

(8) Clicking on 'Map Results' will bring you to the PCBs red hit and blue pass stations in Figures 26.

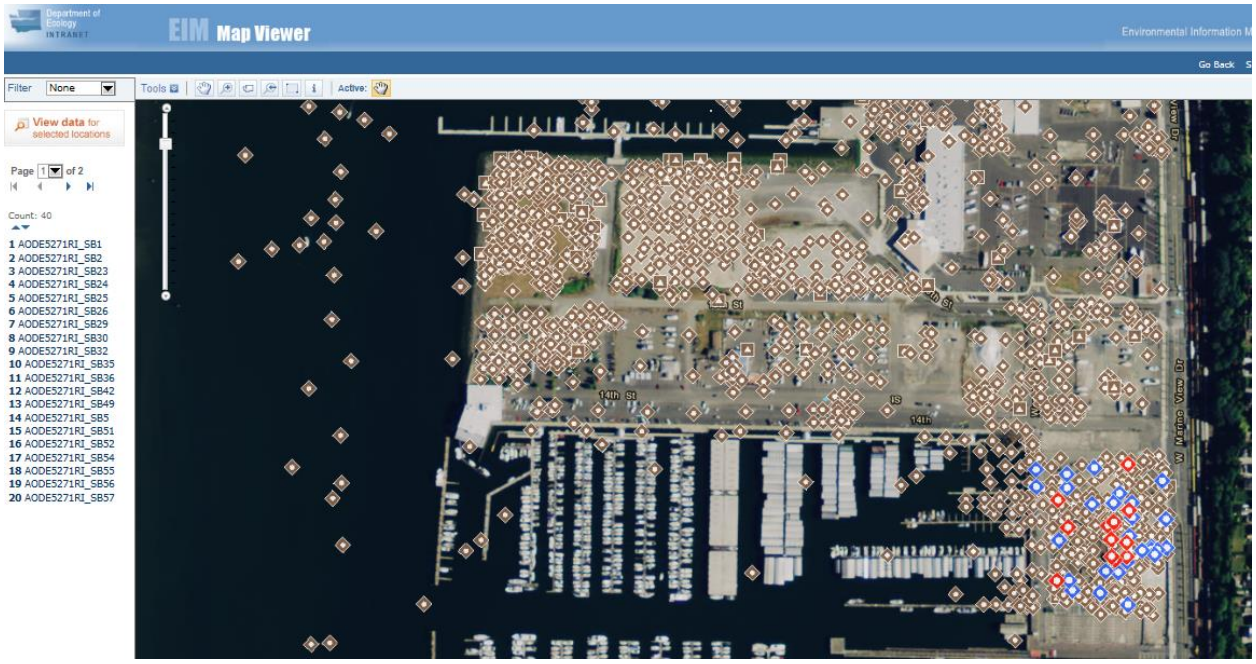

Figure 26 – EIM Map Viewer Page for Analyzed PCBs Soil Chemistry Results

Comparing the maps in Figures 25 and 26 would give you the information on how much PCBs contribute to the hit stations in relation to all the chemistry comparison result hits. PCBs were chosen, because they were identified as potential indicator hazardous substances in the statistical summary spreadsheet.

Note: When you Export Results, the exported files will contain only the filtered results. When you Map Results, only the filtered results show up in the Map.

The filter tool operates on the Chemistry Analysis results grid. The Derived Variable grid is filtered through the radio buttons shown in Listing Options for Derived Variables and using the "*Select*" link provided at the beginning of each row in the Chemistry Analysis results grid.

Results can be sorted based on column values in the chemistry results as well as derived variables grids by clicking on the column header. Sorting can be done with or without applying the filters. If the column values are associated with values in the other columns, the MyEIM sorting algorithm takes this factor into account. For example, since concentrations are associated with unit of measure, MyEIM sorts concentrations by taking into account the unit of measure. Similarly, upper depth and lower depth values are sorted using depth unit of measure.

Note: The sort and filter output feature in MyEIM is especially useful if the sorted/filtered column is dependent on another column as in the above example. In Excel you will need to write a custom sorting/filtering macro or code to achieve the same result.

CUSTOMIZING YOUR ANALYSIS

Eventually, you may want to define cleanup criteria of your own with chemicals and criteria values different from those found in the Standard Cleanup Criteria list.

MyEIM analysis allows you to create “User Defined Cleanup Criteria” by either copying existing standard criteria or, by creating new criteria. If you copy existing criteria, you can always alter your copy without affecting the original standard.

If you defined new criteria, you can modify it. You can add a new constituent, delete or modify each of the constituents. There are three types of constituents: chemicals, derived variables, and user defined derived variables.

Complete lists of chemicals and standard derived variables are already available in MyEIM for you to choose from. You can define your own customized derived variables and add to the criteria list. In this section we shall create user defined criteria and user defined derived variables.

EXERCISE 6: CREATING CUSTOM CLEANUP CRITERIA

(1) Let's use the 'Analysis' link through MyEIM Home page to navigate to the criteria page. Open MyEIM in a new browser window and Click on Analysis Link.

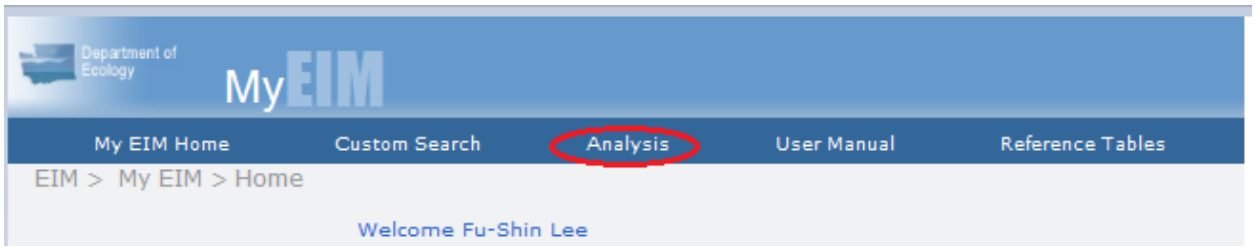

Figure 27 – Link at MyEIM Home Page to Cleanup Criteria page.

(2) In the 'Analysis Home' page, click on Chemistry Criteria.

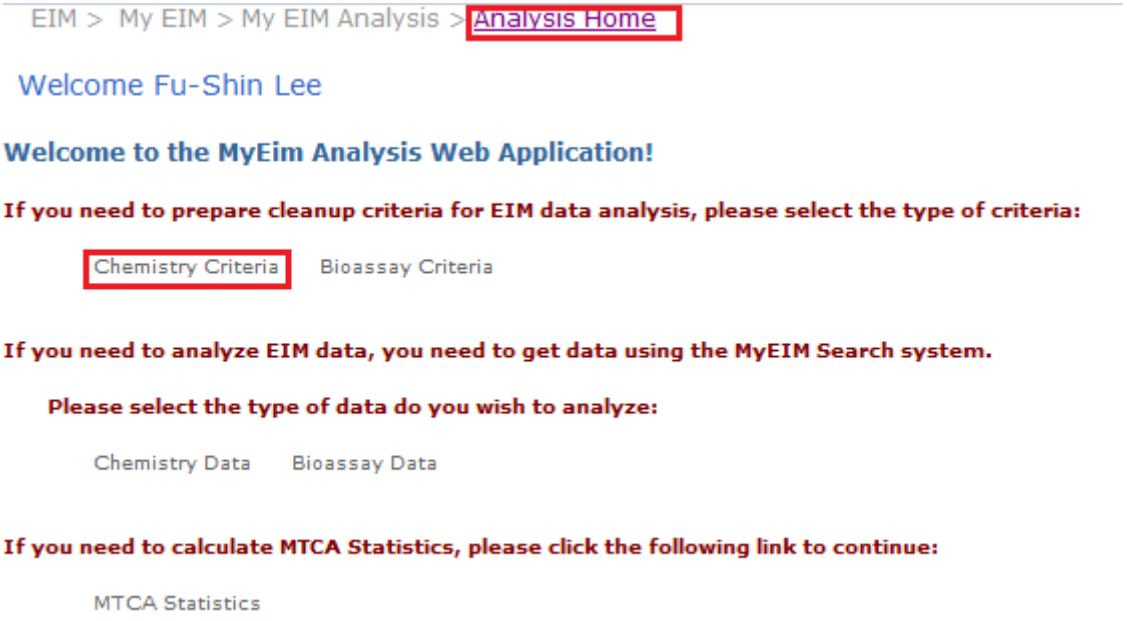

Figure 28 – MyEIM Analysis Home page.

(3) From the Choose Comparison Criteria page, select the User Defined Cleanup Criteria tab. If this is the first time you've clicked this tab, a message informs you to "Please make a copy of the Standard Cleanup Criteria that you want to see in this tab or Add a new one....." Notice no criteria are listed.

Figure 29 - Empty User Defined Cleanup Criteria

(4) MyEIM will prompt you to create a new parameter if there were no cleanup parameters created before. If no cleanup parameters exist, go back to the first Standard Cleanup Criteria tab. To the right of each list item is a *Copy* button . Clicking the *Copy* button creates a copy of the definition under your profile for modification. If you have already created criteria before, click on the green button "New Criteria" to add new criteria.

(5) Create a new criteria set by giving it a name "MTCA training criteria" and then save it by clicking on the 'floppy disk' icon .

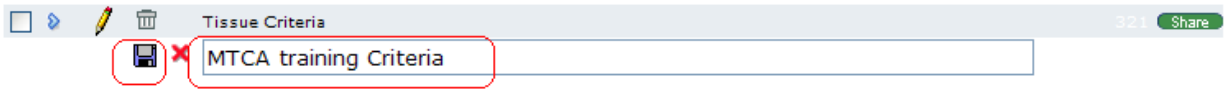

Figure 30 –Name to new Cleanup Criteria

(6) MyEIM will prompt you to input the constituents. Select Chemical in the Constituent Type, Mercury as constituent, UOM as mg/kg, 'dry' basis and a concentration of 1.2. You may also optionally add a comment. Save this as cleanup parameter for chemical Mercury by clicking on the 'floppy disk' icon .

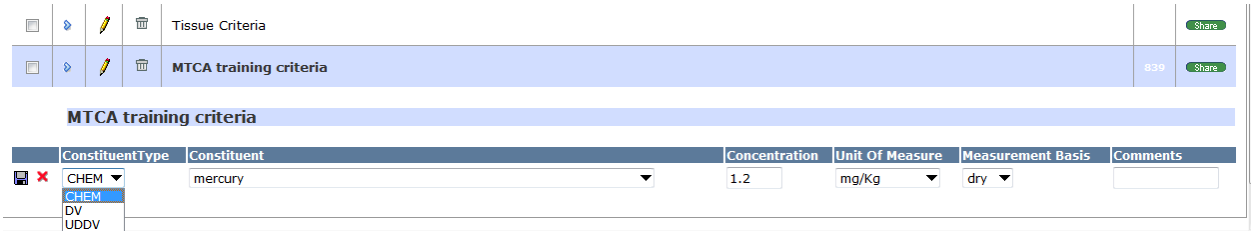

Figure 31 – New cleanup parameter added for mercury.

(7) Next, add another cleanup parameter: this time a standard derived variable, by clicking on the green ‘Add Constituent’ button.

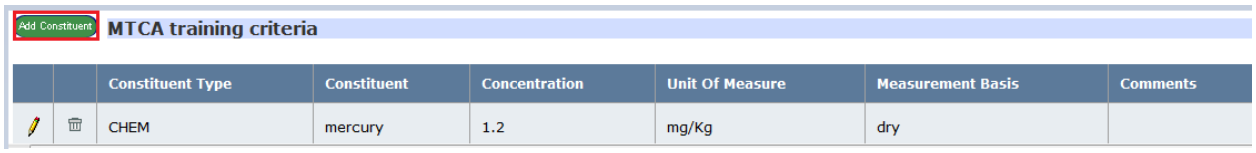

Figure 32 – Adding another cleanup parameter

(8) Add the derived variable PCBs by clicking on the green ‘Add Constituent’ button and providing values as shown below.

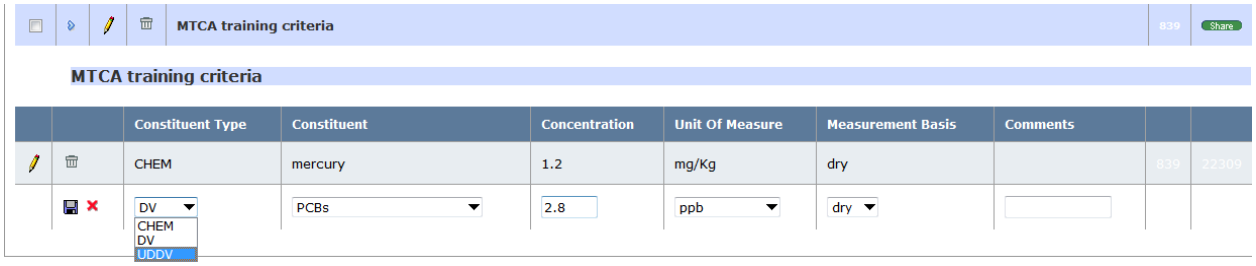

Figure 33 – Add another cleanup parameter, PCB, a derived variable.

When a user defined criteria is selected, its constituents are listed in the grid below. Each constituent can be edited by clicking on the *pencil* icon. The *pencil* icon disappears and is replaced by a *Save disk* icon and a *Cancel red X* icon. You’ll notice there is also a *Delete trash can* icon. After making your change, be sure to select Save.

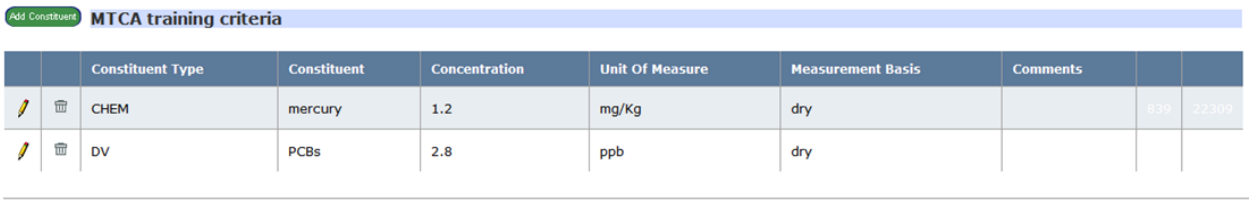

Figure 34 – Save your cleanup parameter.

(9) Go to MyEIM home page and click on ‘ Run’ by the Query you saved “A chemistry soil data check” under ‘My Custom Searches’ section ‘Chemistry’ tab.

(10) Click on ‘*Analyze Data’* in query results page.

(11) Click on the User Defined Cleanup Critera tab in the compare results page. Select the "MTCA training criteria" you just created.

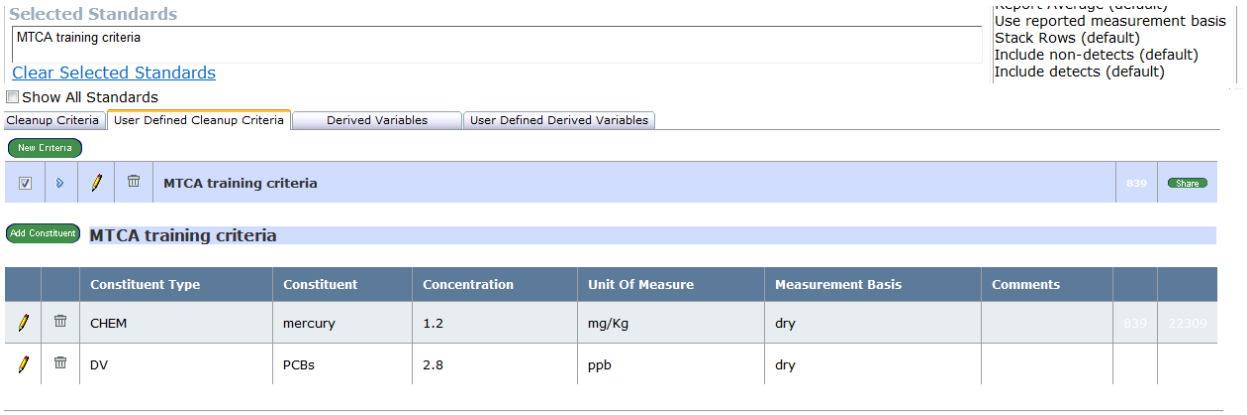

Figure 35 - User Defined Cleanup Criteria selected for comparison.

(12) When you click Compare, your custom User Defined Cleanup Criteria will be used to compare to your searched and calculated data of interest as shown in Figure 36.

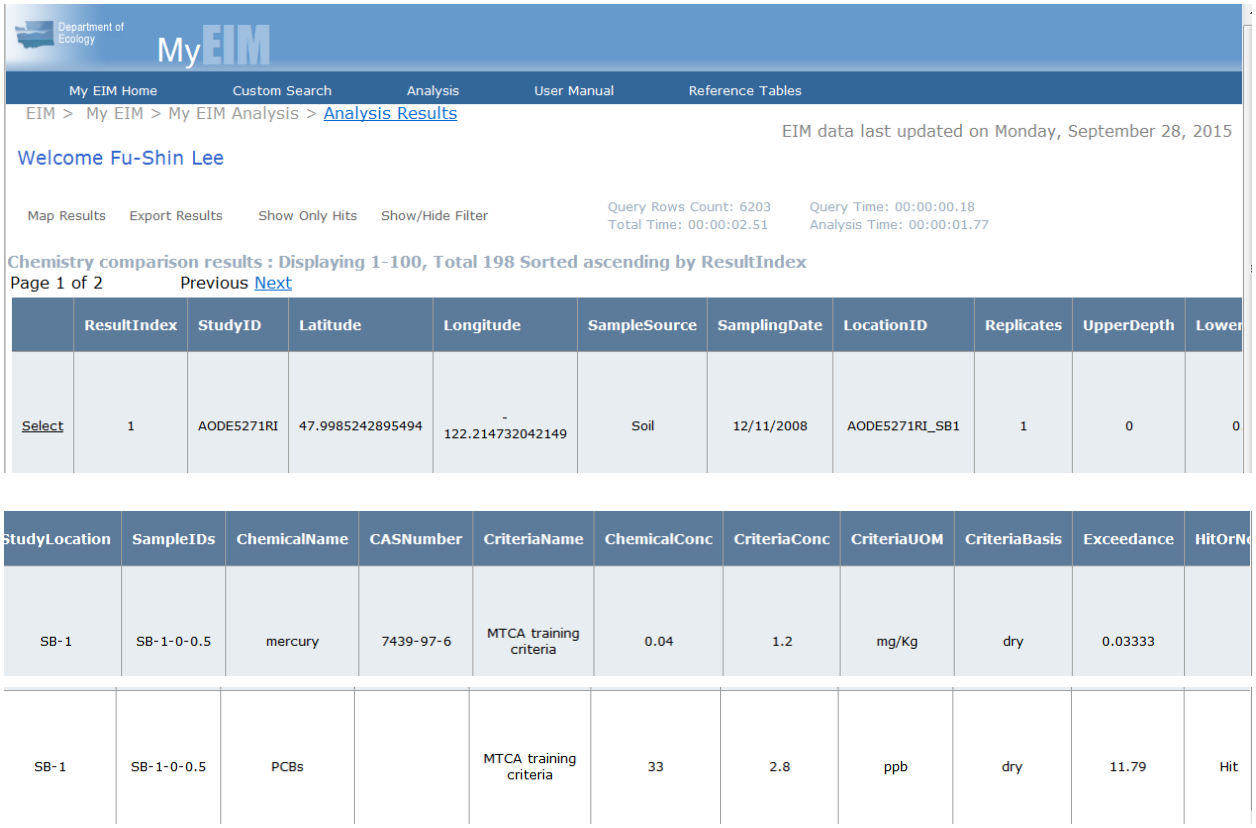

Figure 36 - User Defined Cleanup Criteria used for comparison.

EXERCISE 7: CREATING A CUSTOM DERIVED VARIABLE

(1) Click the User Defined Derived Variables tab. A message instructs you to "Please make a copy of the Standard derived variable that you want to see in this tab…" and a blank user defined derived variable is open and waiting to be defined. Just like the Cleanup Criteria, you can either copy an existing derived variable and alter it, or create a new one.

(2) To Copy and alter an existing Derived Variable: Go to the Standard Derived Variables tab. To the right of each list item is a *Copy* icon. Clicking the *Copy* button creates a copy of the definition under your profile for modification.

(3) Create a new derived variable called "Total EndoSulfan". Click the green "New D.V." button in the User Defined Derived Variable tab as shown in Figure 37.

(4) If this is the first derived variable you are creating, MyEIM will prompt you. Simply enter "Total EndoSulfan" for the new derived variable and a description as "Made up derived variable". Give it a "Detection Limit Scaling Factor" value of 1.0, select PCB Aroclor Sum under Subsidary, enter Testing DV under Comments, and click save icon to successfully save the custom derived variable as shown in Figure 38.

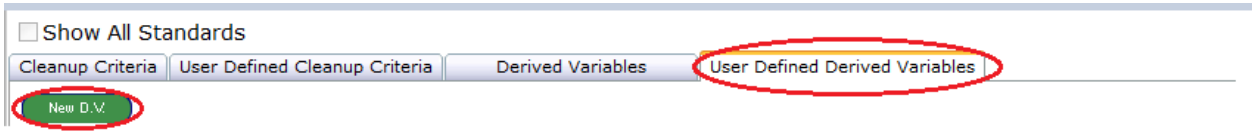

Figure 37 – Create New Derived Variable

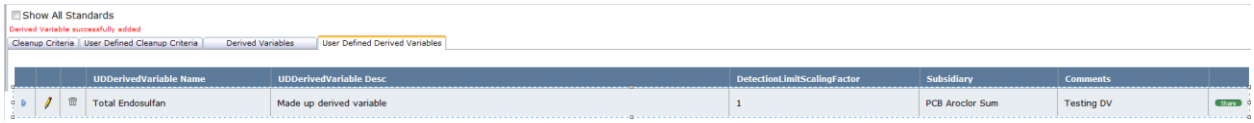

Figure 38- User Defined Derived Variables

The Detection Limit Scaling Factor scales non-detect reported values. If the constituent chemical is a non-detect, then its reported value will be normalized to the unit of measure, normalized to measurement basis if required, scaled down by detection limit scaling factor, multiplied by the toxicity equivalency factor and then added to the total derived Variable Value. Allowed value is in the range 0 <= 'Detection Limit Scaling Factor' <=1.

The new entry has three actions that you can perform. Each is represented by an icon. The name of the new User Defined Derived Variable can be modified by clicking the pencil icon. Change the name to something meaningful and click the Save icon. Derived variable will be saved under name "Total EndoSulfan"

(5) Click blue arrow symbol of the selected Total Endosulfan to display or add the constituent from the Constituent dropdown list. Select alpha Endosulfan from the drop-down list and assign a weight of 1.0.

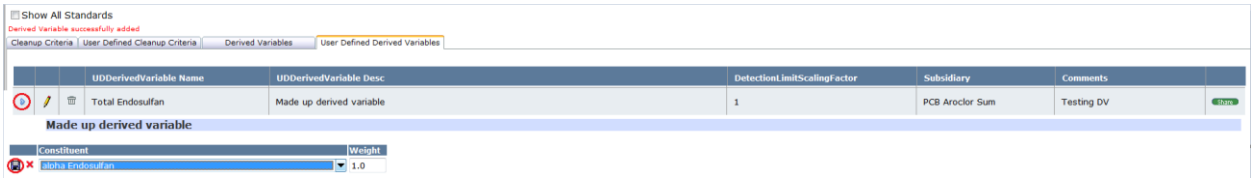

Figure 39– Adding a constituent to user defined derived variable

(6) Clicking the green "New Constituent" button in Figure 40 will enable to add more constituents for beta Endosulfan and Endosulfan Sulfate.

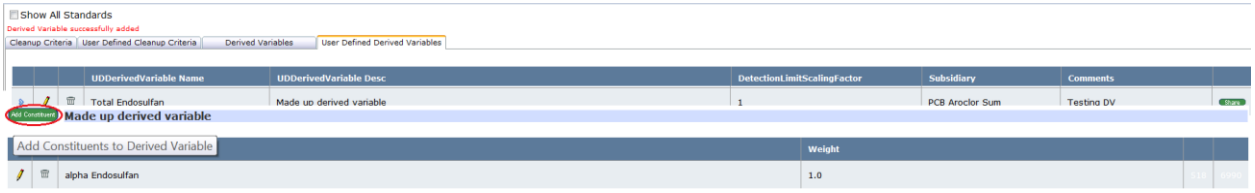

Figure 40- Add more constituents

(7) Each constituent can be edited by clicking on the *pencil* icon. The *pencil* icon disappears and is replaced by a *Save disk* icon, a *Cancel red X* icon, and a *Delete trash can* icon. After making your changes a shown in Figure 41, select the *Save* icon. The weights in this example are fictitious and solely for the purpose of exercise.

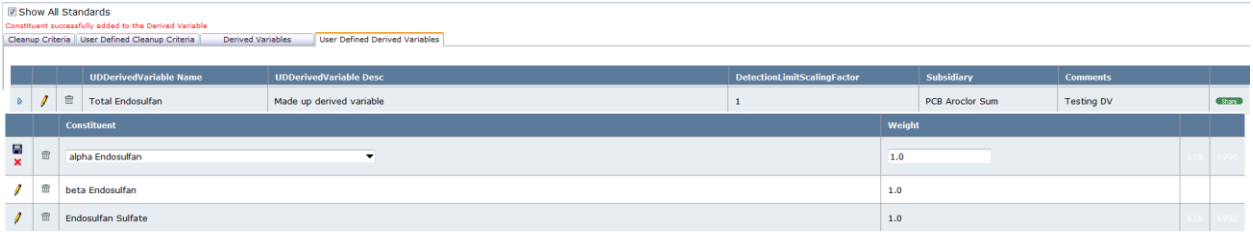

Figure 41 - Constituents listed for a user defined derived variable.

EXERCISE 8: ADDING A CUSTOM DERIVED VARIABLE TO A CUSTOM CRITERION

You will need to add the derived variable you defined in the previous exercise in order to calculate it and compare to a criteria value of your own.

(1) To use your custom derived variable in analysis, switch over to the User Defined Cleanup Criteria tab. Click the green "Add Constituent" button in Figure 42.

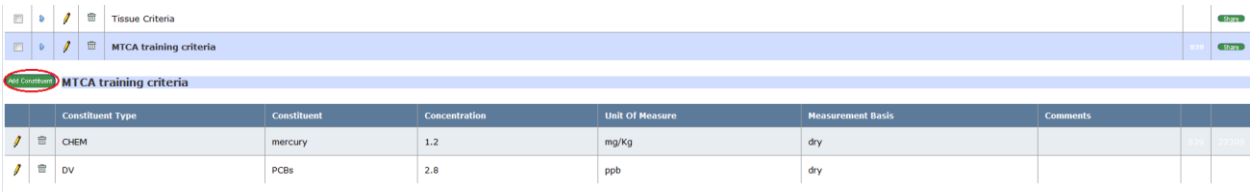

Figure 42 – Expand User Defined Cleanup Criteria to add the new derived variable.

(2) In the Constituent Type drop-down, select "UDDV" and then select the custom derived variable you just created from the constituent drop-down.

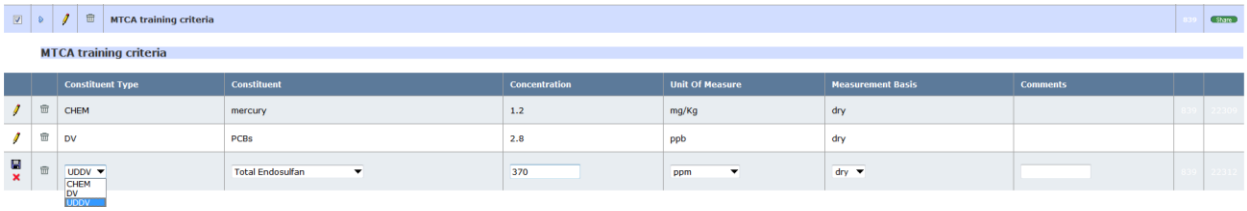

Figure 43 - Selecting a User Defined Derived Variable for a custom analysis.

Set the other properties (Unit of Measure, Measurement Basis, and Concentration) as shown in Figure 43 and then click the save icon.

(3) Then check the checkbox to the left of the cleanup criteria and click the orange "Compare" button.

(4) You have successfully created your custom criteria and used it to analyze DSIP2RI soil data. The new derived variable calculations are highlighted in Figure 44.

StudyLocation	SampleID	ChemicalName	CASNumber	CriteriaName	ChemicalConc	CriteriaConc	CriteriaUOM	CriteriaBasis	Exceedance	HitOrNot
DSIP2-01	DSIP2-01-2.5-4.5	mercury	7439-97-6	MTCA training criteria	0.11	1.2	mg/Kg	dry	0.09167	
DSIP2-01	DSIP2-01-2.5-4.5	PCBs		MTCA training criteria	20	2.8	ppb	dry	7.143	Hit
DSIP2-01	DSIP2-01-2.5-4.5	Total Endosulfan		MTCA training criteria	0.0049	370	ppm	dry	1.324E-05	

DV Name	DV Conc	DV UOM	DV Basis	DV Qualifier	Comment	ChemicalName	CASNumber	WeightedConc	% Contribution
Total Endosulfan	0.0049	ppm	dry	U	OK	alpha Endosulfan	959-98-8	0.0025	0
Total Endosulfan	0.0049	ppm	dry	U	OK	beta Endosulfan	33213-65-9	0.0049	100
Total Endosulfan	0.0049	ppm	dry	U	OK	Endosulfan Sulfate	1031-07-8	0.0049	100

Figure 44 – Results of custom derived variables in custom criteria

Chapter 9: MTCA Statistics

The MyEIM has a built in MTCA statistics engine for analyzing environmental data extracted using the Custom Search application.

OVERVIEW OF MTCA STATISTICS TOOL

The MTCA Statistics tool in MyEIM is statistics engine which is completely redeveloped from 'MTCAstat' tools (SITE971.xls and BCKGD971.xls) of Department of Ecology's Toxics Cleanup Program. New users will need to familiarize with Statistical Guidance for Ecology Site Managers and Supplement S-6. Please refer to the Statistical Guidance to learn in details the MTCA statistical analysis, data flow, decision trees and look up data and also examples on how to use different functions are discussed in the Statistical Guidance.

MyEIM provides a new feature in the MTCA statistics engine, a Potential Indicator Hazardous Substances (PIHS) detection function based on the data you provided. This feature may be used as a preliminary filter in your details data analysis for identifying possible candidates that can be tagged as PIHSs. In Appendix H, the decision tree of PIHS logic and the examples of identifying PIHS are provided.

MyEIM also provides an interface directly into the MTCA statistics engine. Analysis tool also leverages this engine to carry out statistical analysis of sediment, soil, water and tissue chemistry data searched using MyEIM search tool.

In this chapter, you will first get familiar with the MTCA statistics interface to use your own data. Later, this chapter will discuss on how to leverage the engine to analyze EIM's data.

Note: Before we begin, this chapter assumes that you have already learned how to acquire data using the Search application and prepare for analysis to leverage the statistics tool. If you do not have a searched data set to work with, please refer to the previous chapters.

ENTRY POINT TO THE MTCA STATISTICS INTERFACE

MTCA statistics is available online through your MyEIM home page. First navigate to MyEIM portal (Home) page in your browser window.

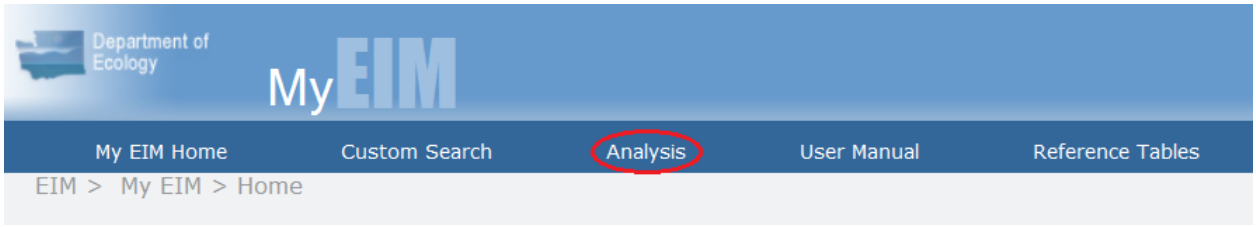

Figure 1 - MyEIM Home Page

Click on the 'Analysis' link as shown in Figure 1.

This will take you to the MyEIM 'Analysis Home' page where further links are provided for Cleanup Criteria pages for both Chemistry and Bioassay, Custom query search tool for Chemistry and Bioassay as well as MTCA Statistics interface. Click on 'MTCA Statistics' link in Figure 2.

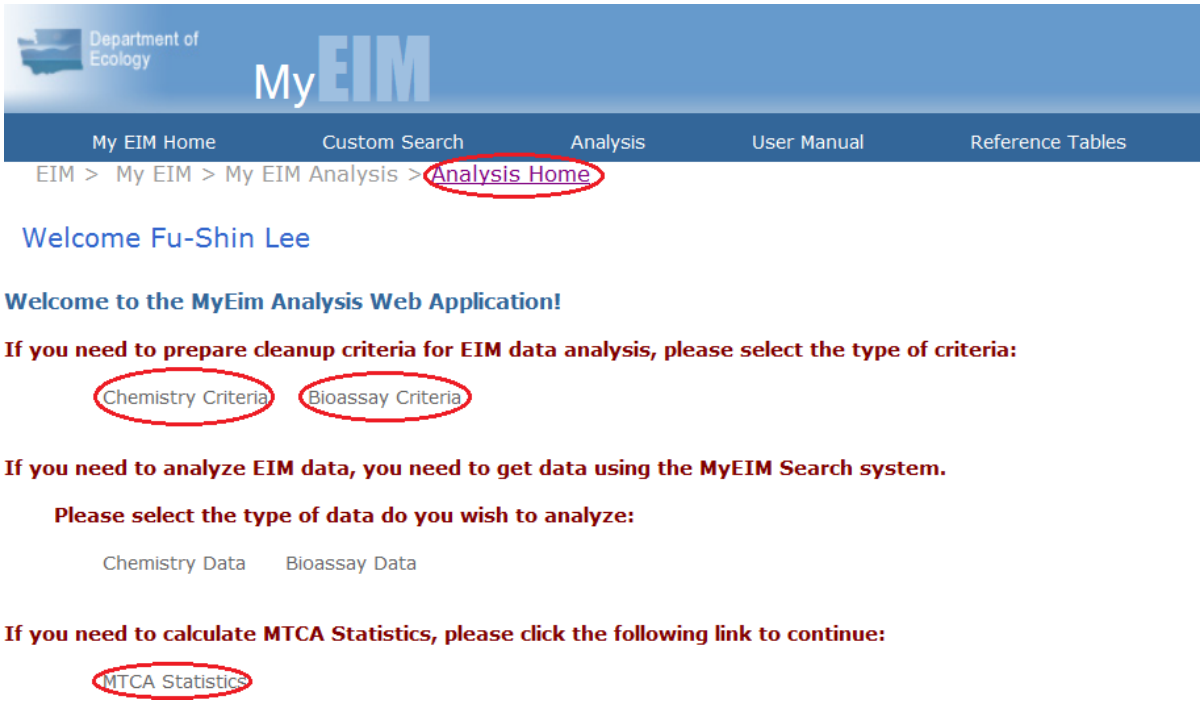

Figure 2 - MyEIM Analysis Home Page

This link will take you directly to the MTCA statistics engine interface.

MTCA STATISTICS INTERFACE

This interface has three panels: Input data, Statistics Parameters and MTCA Results.

Input data text box provides a means to enter your data directly. An example dataset is already provided for you to familiarize with the tool. At the bottom of the input box, is a static message that suggests how to input non-detect concentrations.

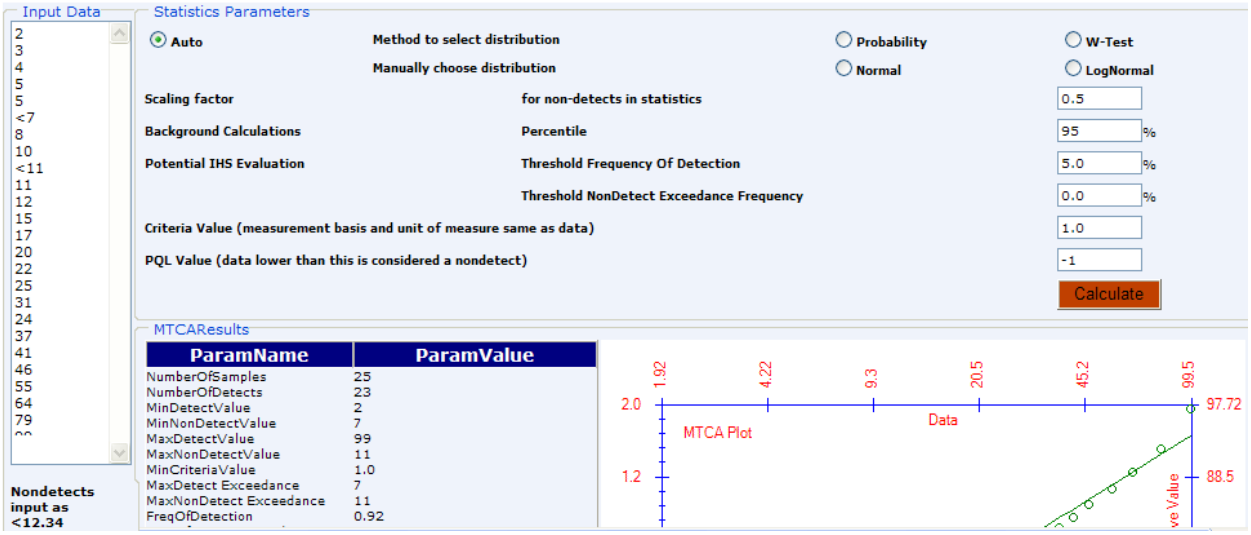

Figure 3 - MyEIM MTCA Statistics Page

The panel “Statistics Parameters” provides settings and tunable parameters based on which the statistics is computed. The tunable parameters include inputs to MTCA Statistics Engine as well as the PIHS function. This panel also has a ‘Calculate’ button to instruct the engine to calculate.

MTCA Results panel is the place holder for statistics output. The output is visible only after statistics is calculated. It has a data grid detailing statistics data and a graph showing analyzed data.

DATA INPUT TO MTCA STATISTICS

You can type the concentration data in directly. It takes in decimals (example 12.34) and also scientific notation (example 1.2E-4).

You can also select a column of data from excel spread sheet and paste directly into the input data box.

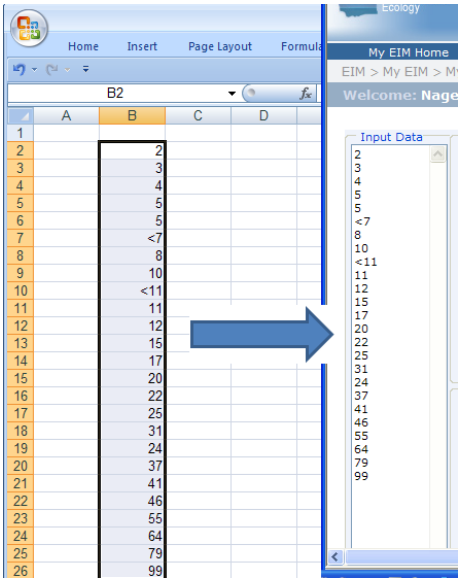

Figure 4 - The MTCA statistics interface can import excel spreadsheet column data

Non-detect data for calculations can be input in four different ways.

- Prefix the concentration value with '<' character.
- Suffix the concentration value with 'U' character. U is a qualifier code in EIM that accompanies a non-detect value.
- Suffix the concentration value with 'ND' characters.
- Provide a Practical Quantitation Limit (PQL) value in the input box in Statistics Parameters panel. All input concentration values that are equal to or less than this PQL value will be tagged non-detects by the engine.

STATISTICAL ANALYSIS OPTIONS

Statistical options are provided through settings and input boxes in the Statistical Parameters panel.

MTCA Statistics will check which of the two statistical distribution profiles, normal or lognormal, your data follows.

You can let the engine find automatically, in this case check 'Auto' radio button which is the default choice. Engine first investigates the probability method, and if unsuccessful, uses W-Test method to find the best matching distribution.

Alternately, you can suggest the engine which of the two routes to follow Probability or W-Test to find the best fit distribution.

You can also force the statistics engine to test against either Normal or Lognormal distributions.

Note: MTCA stat approved only normal and lognormal distributions for analysis. Currently only these two distributions are available for analysis. Toxics Cleanup Program is researching possibility of incorporating nonparametric methods in to the engine. For details refer to Statistical Guidance for Ecology Site Managers, and Supplement S-6.

You can scale the non-detect values by a fractional value between 0 and 1 inclusive, by providing a value in the scaling factor input box. The default value is 0.5 which sets the value to half of the detection limit.

You can enter target percentile for background calculations in the percentile input box.

PIHS function requires a threshold detection frequency, a threshold non-detect Exceedance frequency and a cleanup criteria value for analysis. Statistical panel has input boxes for each of these tunable parameters. Cleanup criteria value will be in the same unit of measure and measurement basis as the input data.

Calculate Button initiates MTCA statistics calculations. The output panel is populated as soon as the calculations are completed.

STATISTICAL OUTPUT

Statistical results are output in a data grid as well as a pictorial representation of the best fit to the distribution. Data grid has two columns: Parameter Name and Parameter Value. In the following, the parameter names are explained.

Number Of Samples is the total number of data points in the input dataset.

NumberOfDetects is the difference between data points and number of non-detects.

MinDetectValue is the lowest detect concentration value.

MinNonDetectValue is the lowest non-detect U qualified concentration value.

MaxDetectValue is the maximum of detect concentration values.

MaxNonDetectValue is the maximum of non-detect U qualified concentration values.

MinCriteriaValue is the criteria value. This interface takes in only one criteria value which is the lowest value.

MaxDetect Exceedance is the ratio of maximum detected concentration to the criteria value.

MaxNonDetect Exceedance is the ratio of maximum non-detect concentration to the criteria value.

FreqOfDetection is ratio of the number of detect samples to total number of samples.

FreqOfDetect Exceedance is the ratio of the number of detect samples that exceed the criteria value to total number of samples.

FreqOfNonDetect Exceedance is the ratio of the number of non-detect samples that exceed the criteria value to total number of samples.

PotentialIHS: Output from PIHS function. It has four possible outputs.

- Yes, the chemical is a PIHS
- No, the chemical is not a PIHS
- No Criteria: not criteria value is provided, hence cannot determine.
- Evaluate: Could not conclude if the chemical is a PIHS based on the information provided. A further evaluation is necessary.

Mean, Median, Mode, Standard deviation (StdDev), Variance, Coefficient of variance (CoeffOfVar), skewness, kurtosis, are regular statistical parameters evaluated by the engine.

NormalR2 and LogNormalR2 are the regression coefficients for fit to normal and lognormal distributions respectively.

Test is the W-Test for sample size <= 50 and D'Agustino's test for sample size > 50.

TestValueN and TestValueLN are test values considering normal and lognormal distributions respectively.

TableValues are look up values for the test.

UCLMethod is the distribution selected by the engine.

UCLValue is upper 95% confidence limit on the mean.

UCL Exceedance is the ratio of the UCLValue to the minimum criteria value. It is calculated only if the UCL value falls within the data value range.

ANOVAPValue Analysis of variance regression F-Distribution value at p=0.05 level.

PercentileValue, 50Percentile, 4X50Percentile, Coefficient of Variance background (CVBckGnd) are outputs from background calculations.

MTCAComments are the messages emanating from MTCA statistics engine.

MTCA Plot:

The two dimensional graph plots the z-score vs. input data if the data confirms to normal distribution. If the data confirms to lognormal distribution, z-score vs. log of input data is plotted. In that case the data is plotted on the top axis in log scale. The vertical axis on the right shows the cumulative value of the distribution.

STATISTICAL ANALYSIS OF MYEIM UPLANDS DATA

MyEIM MTCA statistics engine can take input from MyEIM search application and analyze data by grouping in several different ways. This allows analysis of chemical concentrations, derived variables and user defined derived variables making this engine one of the most powerful online tools for environmental data analysis in all of the government agencies.

Let us take an example and discuss details as we progress in this chapter. First, create a custom query in MyEIM search interface as in Figure-5 to begin.

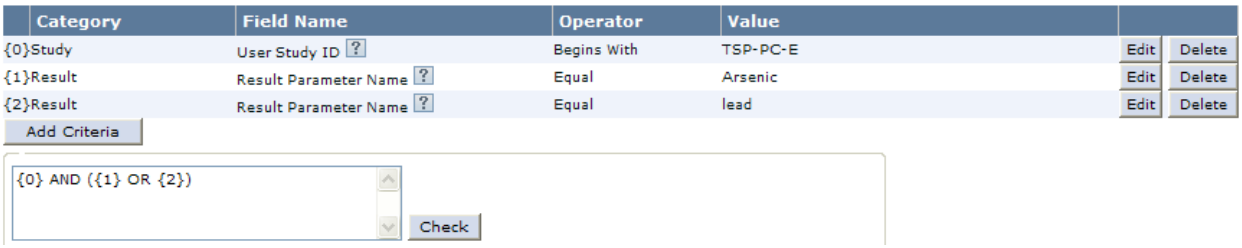

Figure 5 – Custom query to prepare for statistical analysis.

Click on 'Show Data' and then in Query results page on 'Analyze Data'.

In the compare results page, choose MTCA analysis type and select several cleanup standards as shown in Figure 6.

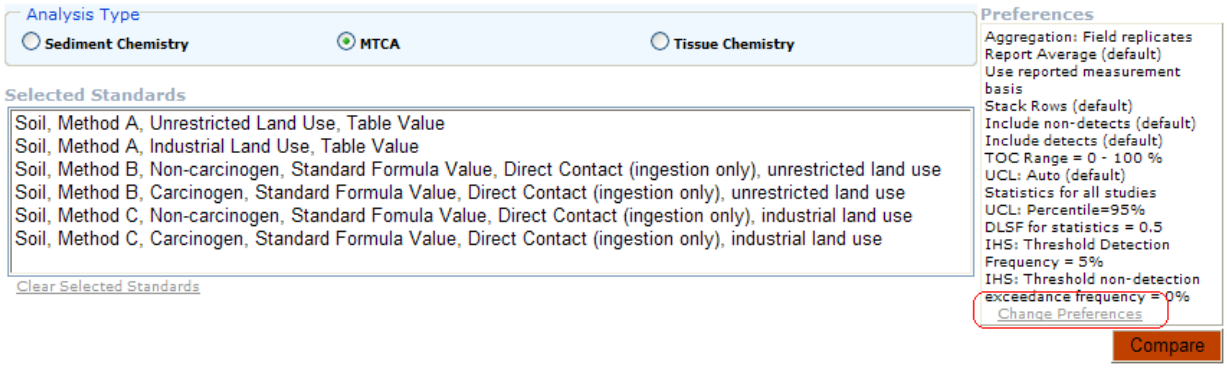

Figure 6 – Select several cleanup criteria for analysis.

The statistics engine's manager module passes query data through data aggregation and criteria comparison modules before calculating statistics. Data aggregation is based on aggregation level, result reporting mode, measurement basis and TOC Range options where applicable, hence you need to familiarize with the data aggregation logic before using invoking statistics in MyEIM.

Aggregated data are compared to all selected criteria when 'No Statistics' default value is set in the statistical preferences panel.

The PIHS module in the statistics engine can take only one criteria value. When statistics is invoked, aggregated data is compared only with lowest criteria value (most stringent criteria) even if you have selected multiple cleanup parameters. Therefore if you select multiple cleanup parameters, the manager sifts through criteria list for each chemical and prepares a distinct list of lowest criteria values for each set of measurement basis and non convertible units of measure that are common in MyEIM data and selected parameters.

Note: In MyEIM, two units of measure are convertible is their dimensions match and they are convertible by a dimensionless factor. For example 'mg/kg' and 'ppm' are convertible set units of measure. Units 'umoles/g' and 'ppm' make a non-convertible set of units of measure because conversion requires additional information of atomic or molecular weight that is chemical dependent. Units 'mg/kg' and 'g/L' are non convertible because conversion requires information on density of the solvent.

MTCA statistics engine takes output of aggregation module and analyzes based on the options you choose from Statistics Parameters panel in the preferences menu. Click on change preferences link in the Preferences box as highlighted in Figure 6.

In the Statistics Parameters panel, 'No Statistics' is chosen by default. In order to invoke statistical analysis, click on an available option in the 'Group by' setting. For MTCA analysis type there are four options: 'All Studies', 'Study', 'Method', and Method, Lab. Select 'All studies' option to identify potential indicator hazardous substances. Select 'Study' and 'Method, Lab' to check if the analysis method and analysis laboratory were entered correctly for the specific study data, the complete data set were submitted, and the data met the specified data quality objectives of the sampling analysis plan, when the data were submitted as a specified study ID for the specified sampling analysis plan.

Group by 'all studies' option will group all concentration values for every chemical in the whole complete search data for each measurement basis and non convertible unit of measure.

Group by 'Study' will group all concentration values for every chemical in each study of the complete search data for each measurement basis and non convertible unit of measure.

Select 'All studies' option. Click 'OK'.

Note: You have already familiarized with other options in the Statistical Parameters panel. The criteria value you input for PIHS module in the MTCA statistics interface now comes from lowest value among cleanup parameters.

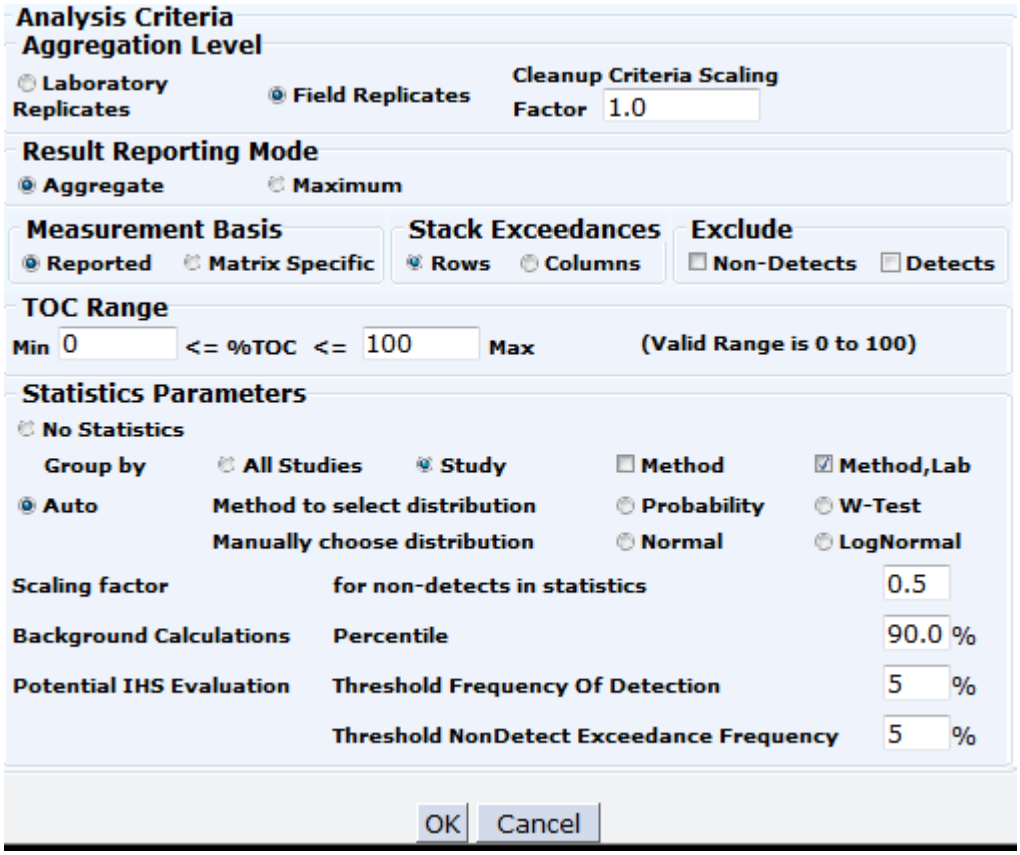

Figure 7 – Click on 'All Studies' or 'Study' to invoke statistics for MTCA analysis type.

Click 'Compare' button.

You will be taken to display results page. This page now has three grids: Criteria Comparison results, Derived Variable and Statistical results. You will need to scroll down the browser window to see statistical output.

Graph	ResultIndex	UserStudyID	ChemicalName	MeasurementBasis	NumberOfStations	Location of Max Concn	NumberOfSamples	NumberOfDetects	CommonUOM
	1	All Studies	arsenic	dry	82	3390200731	166	166	mg/Kg
	2	All Studies	lead	dry	82	8935028960	166	166	mg/Kg

MinDetectValue	MinDetect Qualifier	MinNonDetectValue	MinNonDetect Qualifier	MaxDetectValue	MaxDetect Qualifier	MaxNonDetectValue	MaxNonDetect Qualifier	Criteria Name	MinCriteriaValue
2				350				R_Soil_Meth B_Carc	0.67
7				1900				R_Soil_Meth A_Unrestricted	250

Figure 8a – Statistics output columns.

Figure 8a shows the MyEIM statistical data summary information for each chemical. The first column is Graph. Click on the graph icon on any row to see the MTCA plot for that row. If you click on second row, you will see a graph as in Figure 8b. If 'All studies' option was chosen, this column will show 'All Studies' on each row. For group by option 'Study' each row will show respective Study ID for the data in that row. Chemical name, measurement basis and common unit of measure are the distinct fields associated with the source data used in the analysis.

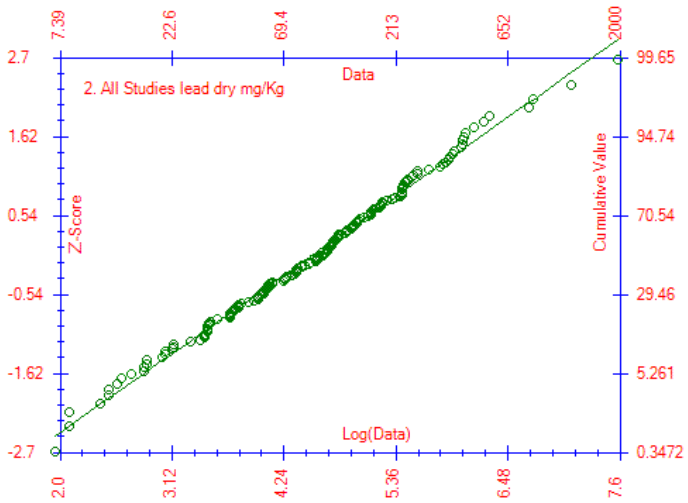

Figure 8b – MTCA Plot title indicates the Result Index, Chemical name, Basis and concentration unit.

Number of stations is the number of sample collection locations pertaining to the data in that row.

CASNumber is a unique identifier assigned by the Chemical Abstract Service to every chemical substance described in the open scientific literature.

Location of maximum concentration is the sample location where the maximum concentration was observed for that chemical. If there are more than one location with the maximum concentration, those location ids will be shown together concatenated by a '+' delimiter character in between.

Most of the column names are already discussed in this chapter previously when reviewing MTCA statistics interface. At that time these column names were listed in a data grid column called Parameter name. Here you will review the column names that were previously not covered.

AnalysisLab is the laboratory analyzing the chemical. This column will only be displayed when Method, Lab is checked at the Preferences.

AnalysisMethod is the analysis method used by the laboratory and specified in the sampling analysis plan or quality assurance project plan to analyze the chemical. This column will only be displayed when Method or Method, Lab is checked at the Preferences.

MinRL is the minimum reporting limit of the chemical for the specific study if Study is checked at the Preferences or for all the studies if All Studies is checked at the Preferences.

MaxRL is the maximum reporting limit of the chemical for the specific study if Study is checked at the Preferences or for all the studies if All Studies is checked at the Preferences.

MinDL is the minimum detection limit of the chemical for the specific study if Study is checked at the Preferences or for all the studies if All Studies is checked at the Preferences.

MaxDL is the maximum detection limit of the chemical for the specific study if Study is checked at the Preferences or for all the studies if All Studies is checked at the Preferences.

MinDetectQualifier is the qualifier code associated with minimum detect value in the data.

MinNonDetectQualifier is the qualifier code associated with minimum non-detect value in the data.

MaxDetectQualifier is the qualifier code associated with maximum detect value in the data.

MaxNonDetectQualifier is the qualifier code associated with maximum non-detect value in the data.

Criteria Name is the name of the criteria with lowest criteria value for the chemical for the basis and unit listed in that row.

Minimum criteria value in this case is the lowest criteria value among the selected cleanup criteria.

You have already familiarized previously with remaining column names in the statistical output.

Note: MyEIM MTCA statistics engine will compute statistics for all chemicals for your preferences settings even if you do not select any criteria for comparison. The criteria are used only for PIHS determination module in the statistics engine.

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EXERCISE 1: STATISTICS USING USER DEFINED CRITERIA

In this exercise, you will study statistics on chemicals and calculated derived variables using your custom criteria and determine PIHS using your cleanup criteria value.

Create a custom query as follows:

ID	Category	Field Name	Operator	Value	
{0}	Sample	Sample Source	Equal	Soil	Edit Delete
{1}	Study	Study ID	Equal	DSIP2RI	Edit Delete

Figure 9 – Create a custom search for statistical analysis.

Get the query data and proceed to analysis.

MTCA training criteria

Add Constituent **MTCA training criteria**

		Constituent Type	Constituent	Concentration	Unit Of Measure	Measurement Basis
		CHEM	mercury	1.2	mg/Kg	dry
		DV	PCBs	2.8	ppb	dry
		UDDV	Total Endosulfan	370	ppm	dry

Figure 10 – Select the custom criteria you previously developed.

Select the user defined criteria you had created previously named "MTCA criteria" shown in Figure -10 containing three chemicals, one single chemical, one derived variable and one user defined derived variable.

Statistics Parameters

No Statistics

Group by All Studies Study

Figure 11 – Select Group by All Studies.

Select Group by option 'All studies' as shown in Figure 11 and click 'OK' in the preferences menu. Click Compare button. Review Statistics output for mercury, PCBs and total endosulfan.

EXPORTING STATISTICS DATA

When statistics is invoked and statistics is successfully calculated, a new export link appears in the analysis results page as shown in Figure -12.

Figure 12 – New export Statistics link appears when statistics is calculated.

Click on the Export Statistics link. A dialog box prompt in Figure 13 will confirm the file download.

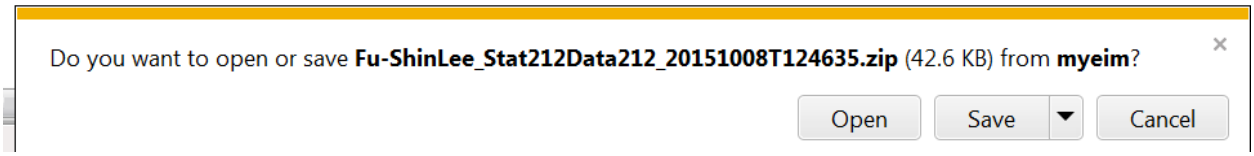


Figure 13a – Downloaded Data Zip File for Statistics Results.

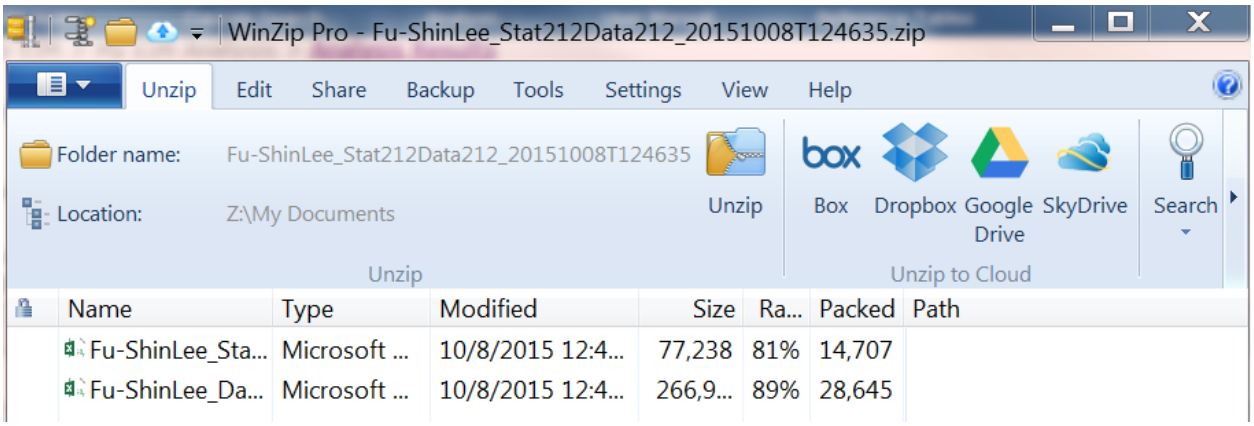


Figure 13b – Downloaded Data Spreadsheet Files.

Clicking on 'Open' in Figure 13a will show you the following chemistry spreadsheet files. You can double click on the file in Figure 13b to view and save this spreadsheet in your folder.

This zip file contains two CSV files. One of the CSV files represents the Statistics Summary Output results exactly as shown in the statistics results grid. The second CSV file contains statistics source data. The CSV file can be easily opened using Excel. The file contains for each chemical, the distinct fields (Chemical name, user study id, basis, unit of measure) that identify

each row in the statistics output grid and all concentrations used in MTCA statistical analysis. This file is provided for exportability to study using other available statistics software.

STATISTICAL ANALYSIS OF MYEIM TISSUE DATA

MTCA Statistics engine operates on tissue data in the same way as MTCA data or sediments data. Two fields specific to tissue data (taxon name and tissue type) are used as constraints for sub grouping data. Overall, MyEIM analysis tool provides two data reduction rules (aggregate, maximum), two aggregation levels (laboratory replicate, field replicate), two ways to assign basis (reported, matrix specific), and MTCA statistics tool provides six different statistics modes (Group by All studies, Study, with or without Taxon Name or Taxon Name + Tissue Type) when used together in combinations provide 48 different ways at high level for tissue statistics and various fine tuning capabilities at a deeper level (statistics distribution choices, tunable statistical and IHS parameters) in additions to output options. This makes MyEIM a very powerful analysis tool to analyze EIM's tissue data, develop criteria as well as perform routine quality assurance/quality control (QA/QC) and statistical analysis. As usual, MyEIM provides default values and selections are provided for novice users.

Let us start with a tissue query (use different WIRA numbers to process search faster) as shown in Figure 14 to explore these statistics options:

ID	Category	Field Name	Operator	Value	
{0}	Sample	Sample Source	Equal	Animal Tissue	Edit Delete
{1}	Location	WRIA Number	Less Than or Equal	19	Edit Delete
{2}	Groups	EIM Parameter Group	Equal	PCBs (Polychlorinated biphenyls)	Edit Delete

Figure 14 – Build a custom query for tissue analysis.

Get the data and proceed to analysis. Select the tissue criteria you had defined previously.

Tissue Criteria Share

MTCA training Criteria Share

Add Constituent **Tissue Criteria**

Constituent Type	Constituent	Concentration	Unit Of Measure	Measurement Basis	Comments
CHEM	arsenic	20	ppm	wet	
DV	PCBs	5.4	ug/Kg	wet	
UDDV	Tissue cPAH-TEQ	1.5	ug/Kg	wet	CalEPA05

Figure 15 – Build a custom query for tissue analysis.

In the change preferences options, , use default laboratory replicate level aggregation, and in statistics parameters panel Group by ‘All Studies’ option and select also subgroup by ‘Taxon, Tissue Type’.

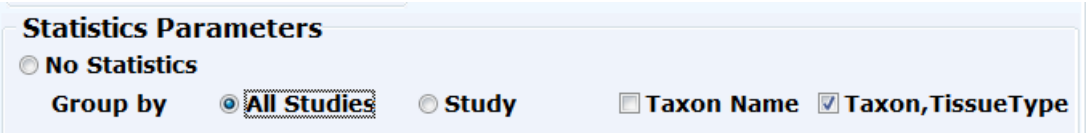
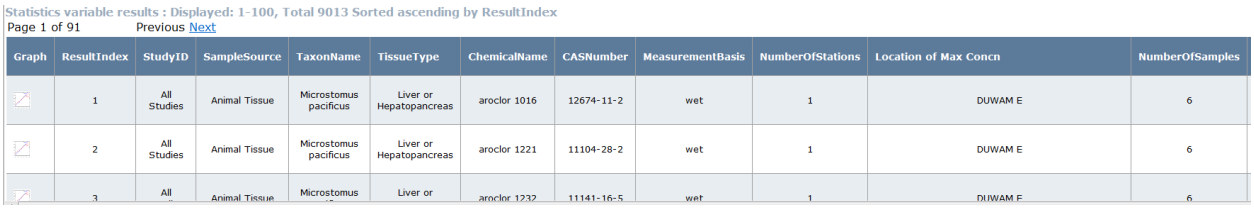


Figure 16 – Select All Studies and Taxon Name grouping.

Click ‘OK’ and then Compare.

In the display results page scroll down to the bottom grid to review statistics output. Since you have grouped statistics by All Studies, Taxon Name, and Tissue Type will appear in the statistics output as shown in Figure 17. All other columns will be same as in MTCA analysis except Analysis Method and Analysis Lab.


Statistics variable results : Displayed: 1-100, Total 9013 Sorted ascending by ResultIndex
Page 1 of 91 Previous Next

Graph	ResultIndex	StudyID	SampleSource	TaxonName	TissueType	ChemicalName	CASNumber	MeasurementBasis	NumberOfStations	Location of Max Concn	NumberOfSamples
	1	All Studies	Animal Tissue	Microstomus pacificus	Liver or Hepatopancreas	aroclor 1016	12674-11-2	wet	1	DUWAM E	6
	2	All Studies	Animal Tissue	Microstomus pacificus	Liver or Hepatopancreas	aroclor 1221	11104-28-2	wet	1	DUWAM E	6
	3	All	Animal Tissue	Microstomus	Liver or	aroclor 1232	11141-16-5	wet	1	DUWAM E	6

Figure 17 – Additional column Taxon Name and Tissue Type in the statistics output.

EXERCISE 2: STATISTICAL BY STUDY, TAXON AND TISSUE TYPE

Get the query results as for tissue data as discussed in previous pages and select the custom criteria you had created for tissue analysis.

In the change preferences options, select field replicate level aggregation, and in statistics parameters panel Group by 'Study' option and select subgroup category 'Taxon ,Tissue Type'.

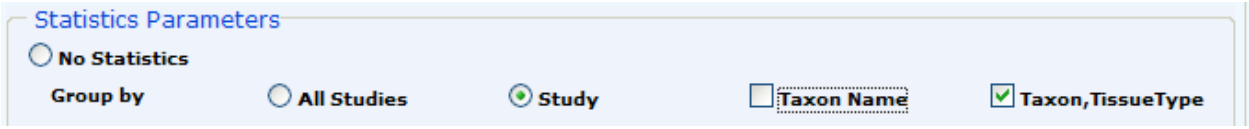


Figure 18 –Select grouping for tissue statistics.

In the change preferences options, select Group by Study option and select also subgroup by 'Taxon ,Tissue Type'. Click 'OK' and then 'Compare'

In the display results page scroll down to review statistics output. Since you have sub grouped statistics into study, taxon name and tissue type two additional columns will appear in the statistics output, namely taxon name and tissue type. All other columns will be same as in MTCA analysis.

Graph	ResultIndex	UserStudyID	TaxonName	TissueType	ChemicalName	MeasurementBasis	NumberOfStations	Location of Max Concn	NumberOfSamples
	5	PSAMPfis	Microstomus pacificus	Liver	aroclor 1248	wet	1	DUWAM E	2
	6	PSAMPfis	Microstomus pacificus	Liver	aroclor 1254	wet	1	DUWAM E	2
	7	PSAMPfis	Microstomus pacificus	Liver	aroclor 1260	wet	1	DUWAM E	2
	8	PSAMPfis	Microstomus pacificus	Liver	pcbs	wet	1	DUWAM E	6
	9	PSAMPfis	Microstomus pacificus	Muscle	aroclor 1242	wet	1	DUWAM E	2
	10	PSAMPfis	Microstomus pacificus	Muscle	aroclor 1016	wet	1	DUWAM E	2
	11	PSAMPfis	Microstomus pacificus	Muscle	aroclor 1221	wet	1	DUWAM E	2

Figure 17 –Select grouping for tissue statistics.

Note: When you group by Taxon and Tissue Type, two additional rows for Taxon Name and Tissue Type will appear in the export statistics source data file to indicate another distinct data field that identifies statistics data source.

Appendix A: MyEIM Access

For Intranet and Internet MyEIM Access to MyEIM Home Page

INTRANET ACCESS TO MYEIM

For Ecology intranet users, you can access MyEIM home page by clicking on MyEIM under Quick Links of TCP intranet home page in Figure A-1, or Ecology EIM intranet home page in Figure A-2.

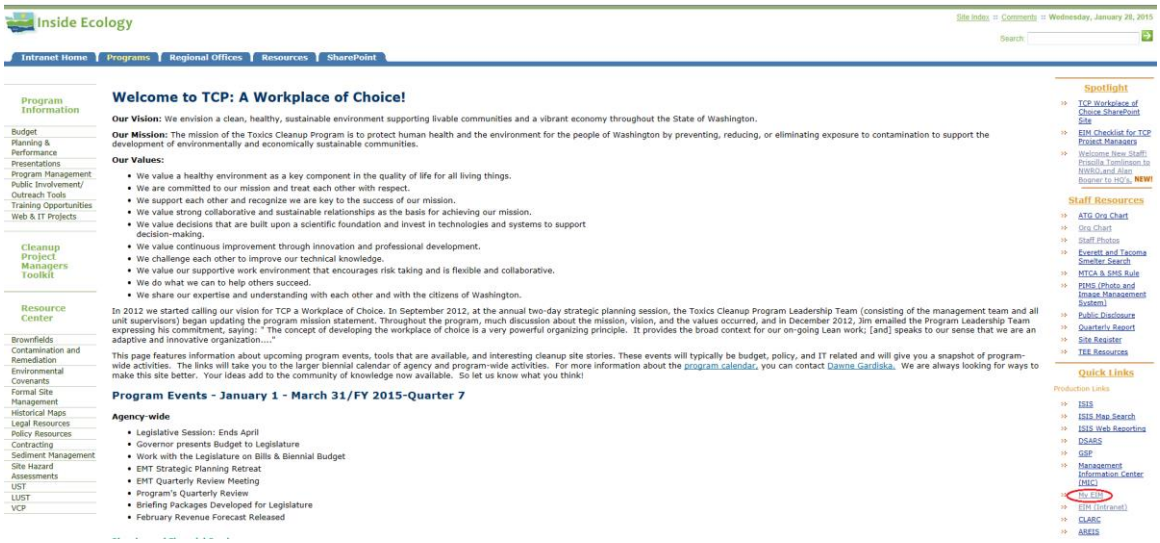


Figure A-1 – MyEIM Access in TCP Intranet Home Page

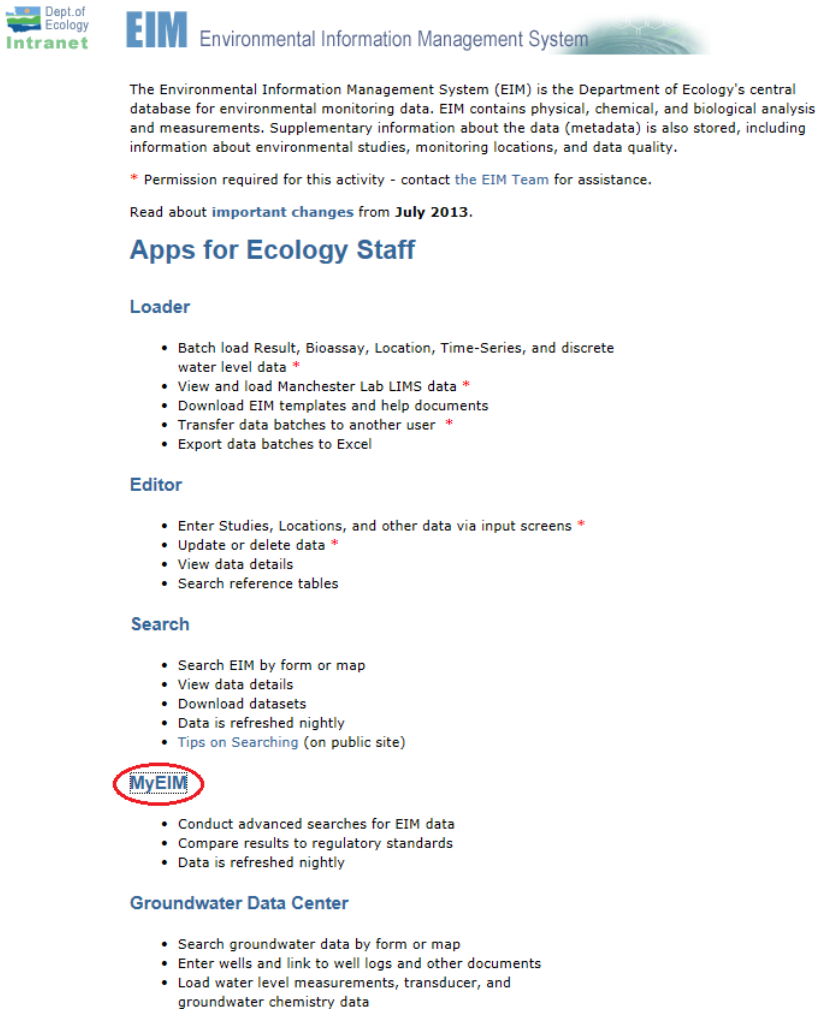


Figure A-2 – MyEIM Access in Ecology EIM Intranet Home Page

INTERNET ACCESS TO MYEIM THROUGH SECURE ACCESS WASHINGTON (SAW)

For Ecology internet users, clicking on the following link will bring you to Secure Access Washington (SAW) 'LOGIN' and 'Create one' page in Figure A-3.
https://secureaccess.wa.gov/

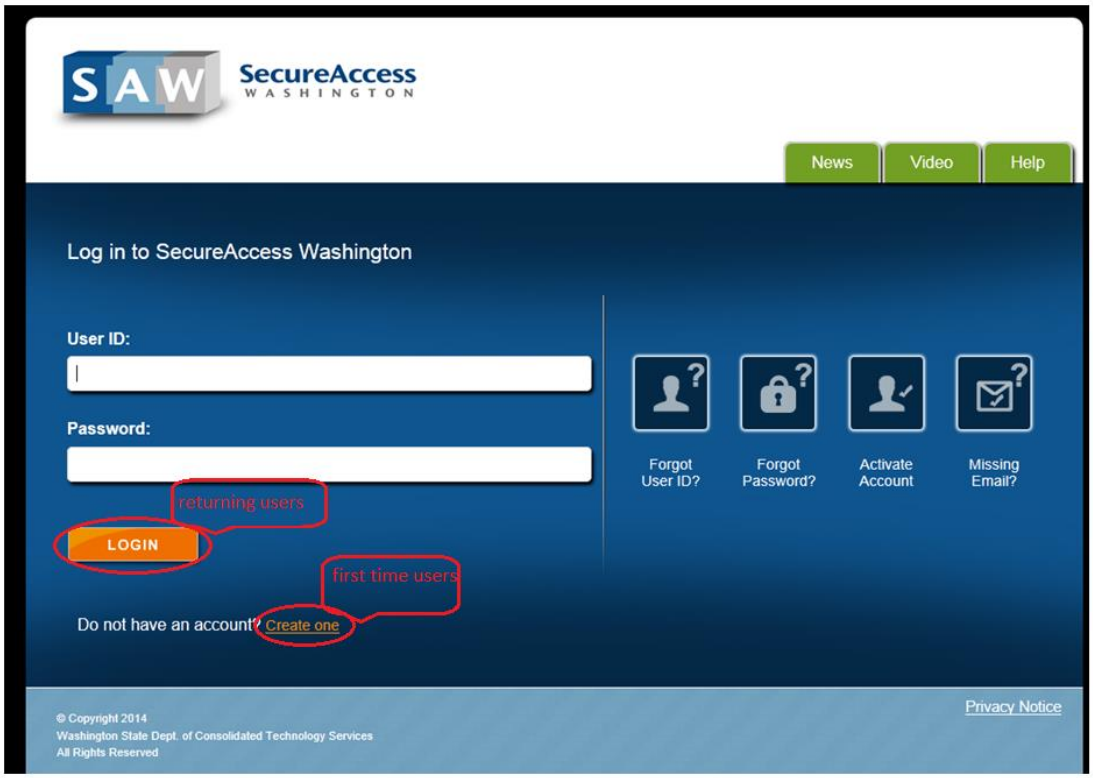


Figure A-3 – LOGIN and Create one on SecureAccess Washington Page

1. Create a SAW account:
   For the first time SAW MyEIM users, clicking on 'Create one' in Figure A-3 will bring you to the following page in Figure A-4 to complete the 6-step process to create a SAW account. After completing the 6-step process, you will receive an approval email.

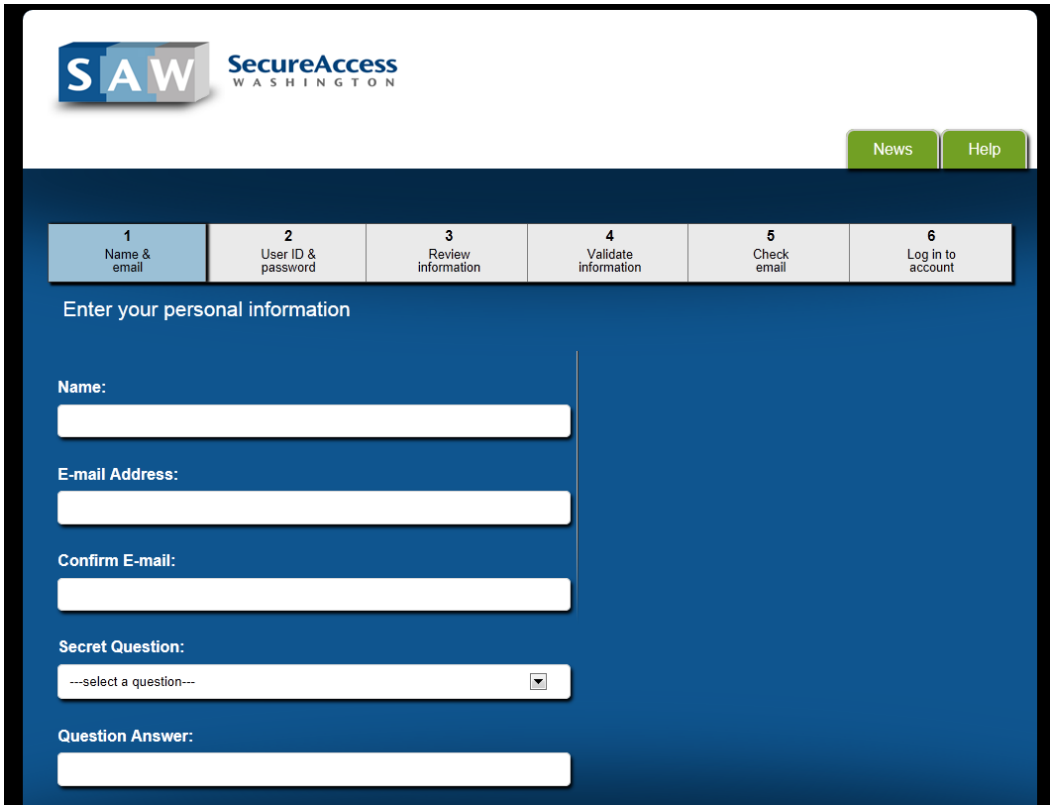


Figure A-4– Create SAW Account Page

2. Add MyEIM service:

   Logging in to SAW by clicking on the link provided in your approved email will bring you to the SAW page in Figure A-5. Select 'Add a New Service', 'Department of Ecology' from the agency list, and 'MyEIM' from the service name list. Clicking on 'Apply' will bring MyEIM under 'My Services' tab as shown in Figure A-5. Now, you are the returning MyEIM SAW user.

Figure A-5 – MyEIM on SecureAccess Washington Page

3. Log in MyEIM through SAW:

   For returning MyEIM SAW user. Enter User ID and Password and click on 'LOGIN' in Figure A-3 will bring you to the page as shown in Figure A-5. Clicking on 'MyEIM' in Figure A-5 will bring you to MyEIM home page.

Appendix B: Troubleshooting Intranet Access to MyEIM

Using Microsoft Internet Explorer

CONFIGURING BROWSER SETTINGS

How to verify Microsoft Internet Explorer browser settings is set to access MyEIM for Intranet access.

1. Open Internet Explorer

2. Choose Tools > Internet Options from the menu bar. The Tools menu is available from the command bar (right-click from the existing bar to access the command bar if it's not visible).

3. Select the Advanced tab at the top right of the Internet Options dialog

4. Scroll to the bottom of the Settings list and ensure that "Enable Integrated Windows Authenticate (requires restart)" is checked.

5. Close and re-open Internet Explorer and navigate to http://myeim. If you still cannot access MyEIM, contact the MyEIM technical support at myeim@ecy.wa.gov.

Appendix C: Bioassay Analysis

SUMMARIZED CHANGES FOR 2014 SPRING MYEIM UPDATES

- Freshwater Bioassay standards have been updated per the 2013 updated SMS bioassay criteria.
- In the Cleanup Criteria list, the Endpoint Code for growth now displays as "GROW"; previously, it would display as "GROW/MORT".
- Information about the reference is now reported in the results even if the analysis is not performed for some reason (i.e. failed QA). Previously, the columns containing information about the reference would just contain "Not Available" even though the reference information was known.
- Fail option was added to RefQA field when Reference QA failed. Before this update, two options, Not Available and Pass, existed in RefQA field, and Not Available was noted when Reference QA failed. This update provided the correct information for Fail, Not Available, and Pass in RefQA field.
- When Reference QA failed or is not available and Control QA passed, the test sample results would be compared to negative control. This business logics was not included in the default bioassay analysis before this update, and the bioassay summary table would show a lot of Not Available in reference section and failedQA in StatHit and IsHit fields.
- When test sample results are compared to negative control, CompareTo field in the bioassay summary table would note Neg Ctl.
- Comment field in the bioassay summary table would specify QA deficiency in the following display for easy interpretation:

    Batch not analyzed

    Batch has no reference samples

    Batch has no control Sample

    All References fail QA

    QA Override applied to compared Reference

    Control QA Failed

    Control QA Override applied

    Test Sample variance is zero

    Control Sample variance is zero

    Reference Sample variance is zero

[Various error messages when something goes wrong, like divide by zero]

- The following fields have been added to the Bioassay Summary table.
    - MatchedRef: Reference sample ID selected for reference data analysis
    - RefCriteria: Reference formula and criteria value
    - RefNumeric: Calculated value of reference formula
    - CtrlCriteria: Control formula and criteria value
    - CtrlNumeric: Calculated value of control formula
    - TestCriteria: Test formula and criteria value
    - TestNumeric: Calculated value of test formula
    - Source: Sample Source
    - SpeciesTSN: Bioassay Taxon TSN
    - Treatment: Bioassay Treatment Code
    - UpperDepth: Field Collection Upper Depth
    - LowerDepth: Field Collection Lower Depth
    - DepthUnit: Field Collection Depth Units
    - Method: Bioassay Method Code
    - Lab: Bioassay Lab Name, the name of the lab performing the bioassay
    - QALevel: Bioassay QA Level Code
    - QAPlanning: Study QA Planning Level
    - Assessment: Study QA Assessment Level
    - Contact: Ecology Contact
    - Program: Ecology Program or Other Responsible Entity
    - StudyName: Study Name

BIOASSAY ANALYSIS LOGICS

Default:

If the batch has no negative control or failed negative control QA, the batch will not be analyzed. If a batch has no reference samples or failed QA for all the reference samples and passed QA for negative control, set the negative control sample to be the reference for each test sample. If a batch does have reference samples, set the reference sample that passes QA and most closely matches the test sample's percent fines to be the reference. The reference sample must pass QA (or have QA overridden for the batch) to be considered for matching.

Override Reference

Clicking this link will override all reference samples that have failed QA for the batches that have passed negative control QA. Re-assign references to all of the test samples in the batch (because the now-overridden reference sample might have a grain size that matches better). This is the equivalent of clicking on all of the red 'F' icons in the 'R' column.

Override Control

Clicking this link will override ALL of the failed negative controls in ALL of the batches to pass QA so that failed negative control QA results are ignored and test samples can be compared to QA passed reference samples, or compared to overridden failed negative control samples when reference QA failed. This is the equivalent of clicking on all the red 'F' icons in the 'C' column.

Set to Control

Clicking this link will override all control samples that have failed QA and match ALL test samples to the control samples instead of reference samples for analysis. This is the equivalent of clicking all of the green '+' icons in the 'SetToControl' column.

DIFFERENCES BETWEEN MYEIM AND SEDQUAL

While developing MyEIM bioassay analysis software modules in 2007, several differences were noted between MyEIM and SEDQUAL. These differences are documented here.

Bioassay analysis tool in MyEIM has been tested to give results consistent with BioStat 2.0 software.

Student's T-Test

MyEIM Student's T-Test operates on original data while SEDQUAL Student's T-Test operates on the deviate data. These differences were observed in the following modules where Student's T-Test is performed:

- LeveneBioStatWay
- Cases where distributions are Normal and Variances are Homogeneous
- Cases where distributions are Not Normal and Variances are Not Homogeneous

In the new tool, Student's T-Test will operate on the data provided to it. Other methods that run Student's T-Test will use original or deviate as required.

MyEIM operates on the deviate data and uses that data in the Student's T-test. SEDQUAL operates on the deviate data and uses deviates of those deviates in the Student's T-Test.

Levene's value compared to two tailed look up value in MyEIM

In the case where distributions are NotNormal and Variances are NotHomogeneous, In MyEIM and in BioStat, LeveneBioStatWay output is compared with two tailed value. In SEDQUAL it is compared with one tailed value, while testing for normality after Rankits. Test for Normality should be a comparison with two tailed value as in BioStat.

Lookup Values

Several look up values were either incorrect or truncated to 2 decimal places in tables of

W-Test Array values (currently up to n=50)

W-Test Critical values (currently up to n=50)

Rankit values (currently up to n = 20)

Mann-Whitney Critical Values (currently up to n1=10 and n2=10)

T-Critical values (currently up to n=30 and n=∞)

Their correct values are stored up to 3 decimal places in MyEIM.

Missing α values provided

While testing for normality and variances in homogeneity, in rare cases, the critical values for α = 0.25 are required. SEDQUAL and BioStat do not have corresponding table values. In MyEIM, these values have been generated through linear interpolation between values for α = 0.1 and α = 0.5 available in literature.

Identical test and reference data

In the case where variances of test and reference populations are zero: and if their averages are not equal, then MyEIM will return false or true depending on the null hypothesis. SEDQUAL has no code in this section.

Percent Silt

SEDQUAL includes Phi-Scale 3-4 in calculation of percent silt value before calculating percent fines. MyEIM does not include Phi-Scale 3-4 in calculation of percent fines.

Power Statistics:

SEDQUAL does not calculate Power statistics for T-Tests. MyEIM allows power calculations for each of the t-tests.

The user input term "minimum detectable difference" ($\mu - \mu 0$) required for power calculations is treated as a part of the bioassay cleanup standard in MyEIM. These values have been adopted from BioStat 2.0 Users Guide.

There are no simple analytical equations available for computing look up values for Power calculation of T-Tests. Actual computation is cumbersome while discrete lookup values may not account for continuity and could lead to truncation errors. MyEIM incorporates excellent functional approximations to inverse cumulative standard normal distribution function and Error function to generate outputs for non-discrete (continuous) values. Following is the literature for more information on these functions.

Approximation to inverse normal cumulative distribution function

Algorithm of Peter J. Acklam: Error in the range of one in billion.
http://home.online.no/~pjacklam/notes/invnorm/index.html

This function is a replacement for the Microsoft Excel Worksheet function NORMSINV. It returns an approximation of the inverse cumulative standard normal distribution function. I.e., given P, it returns an approximation to the X satisfying P = Pr{Z <= X} where Z is a random variable from the standard normal distribution. The algorithm uses a minimax approximation by rational functions and the result has a relative error whose absolute value is less than 1.15e-9.

Pseudo-code: The algorithm below assumes probability p is the input and quantile X is the output. The function is calculated using polynomials fitted for three regions.

Coefficients in rational approximations:

a_1 = -3.969683028665376e+01 c_1 = -7.784894002430293e-03

a_2 = 2.209460984245205e+02 c_2 = -3.223964580411365e-01

a_3 = -2.759285104469687e+02

a_4 = 1.383577518672690e+02

a_5 = -3.066479806614716e+01

a_6 = 2.506628277459239e+00

c_3 = -2.400758277161838e+00

c_4 = -2.549732539343734e+00

c_5 = 4.374664141464968e+00

c_6 = 2.938163982698783e+00

b_1 = -5.447609879822406e+01

b_2 = 1.615858368580409e+02

b_3 = -1.556989798598866e+02

b_4 = 6.680131188771972e+01

b_5 = -1.328068155288572e+01

d_1 = 7.784695709041462e-03

d_2 = 3.224671290700398e-01

d_3 = 2.445134137142996e+00

d_4 = 3.754408661907416e+00

Define break-points.

P_{low}=0.02425

P_{high}=1- P_{low}

Rational approximation for lower region:

For $0 < p < p_{low}$

$q = \sqrt{-2Log(p)}$

$X= (c_1q^5 + c_2q^4 + c_3q^3 + c_4q^2 + c_5q + c_6) / (d_1q^4 + d_2q^3 + d_3q^2 + d_4q + 1)$

Rational approximation for central region:

For $p_{low} <= p <= p_{high}$

$q = p - 0.5$

$r = q^2$

$X= (a_1r^5 + a_2r^4 + a_3r^3 + a_4r^2 + a_5r + a_6)\ q/ (b_1r^5 + b_2r^4 + b_3r^3 + b_4r^2 + b_5r + 1)$

Rational approximation for upper region:

For $p_{high} < p < 1$

$q = \sqrt{-2Log(1-p)}$

$X= (c_1q^5 + c_2q^4 + c_3q^3 + c_4q^2 + c_5q + c_6) / (d_1q^4 + d_2q^3 + d_3q^2 + d_4q + 1)$

Approximation to error function

Ref: Bagby R. J. "Calculating Normal Probabilities." Amer. Math. Monthly **102**, 46-49, 1995. (Uncertainty in the range of less than one in ten thousand)
http://mathworld.wolfram.com/NormalDistributionFunction.html

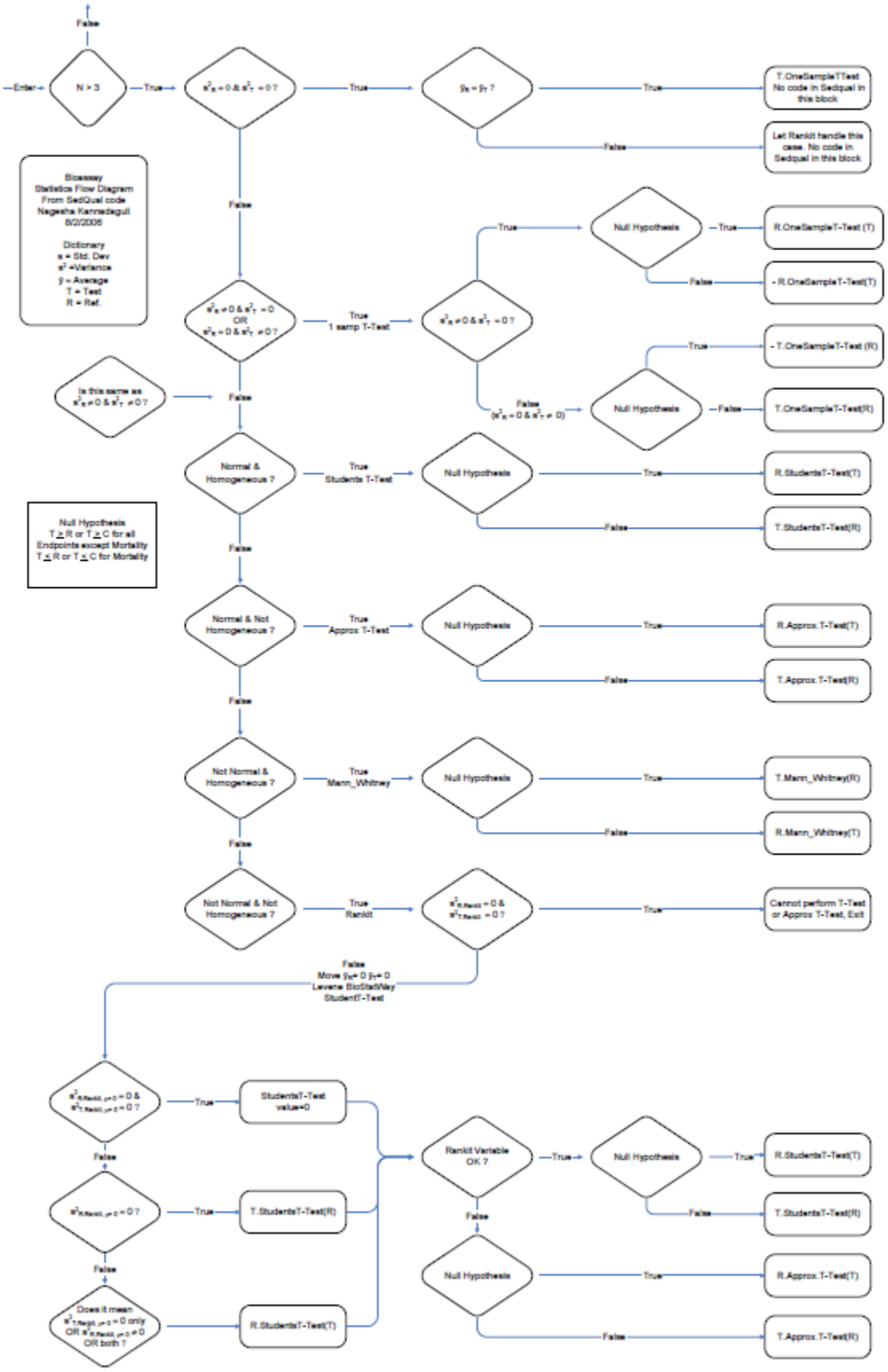
$$\Phi(x) = \frac{1}{2}\left\{1 - \frac{1}{30}\left[7\,e^{-x^2/2} + 16\,e^{-x^2\left(2-\sqrt{2}\right)} + \left(7 + \frac{1}{4}\,\pi x^2\right)e^{-x^2}\right]\right\}^{1/2}.$$

In the power analysis, results of MyEIM, Microsoft Excel functions and BioStat are all consistent at the second decimal place when expressed in percentage.

Appendix D: Bioassay Analysis

Statistical analysis decision tree and logic flow diagram is provided here.

BIOASSAY STATISTICAL ANALYSIS LOGIC


False
Enter
N > 3
True
$s^2_R = 0$ & $s^2_T = 0$?
True
$\bar{y}_R = \bar{y}_T$?
True
T.OneSampleTTest
No code in Sedqual in this block
False
Let Rankit handle this case. No code in Sedqual in this block
Biosssay Statistics Flow Diagram From SedQual code Nagesha Kannadagudi 8/2/2006
Dictionary
s = Std. Dev
s^2 =Variance
$\bar{y}$ = Average
T = Test
R = Ref.
False
$s^2_R = 0$ & $s^2_T = 0$ OR $s^2_R = 0$ & $s^2_T \neq 0$?
True
1 samp T-Test
$s^2_R \neq 0$ & $s^2_T = 0$?
True
Null Hypothesis
True
R.OneSampleT-Test (T)
False
- R.OneSampleT-Test(T)
True
- T.OneSampleT-Test (R)
False
($s^2_R = 0$ & $s^2_T \neq 0$)
Null Hypothesis
False
T.OneSampleT-Test(R)
Is this same as $s^2_R \neq 0$ & $s^2_T \neq 0$?
False
Normal & Homogeneous ?
True
Students T-Test
Null Hypothesis
True
R.StudentsT-Test(T)
False
T.StudentsT-Test(R)
Null Hypothesis
T ≥ R or T ≥ C for all Endpoints except Mortality
T ≤ R or T ≤ C for Mortality
False
Normal & Not Homogeneous ?
True
Approx T-Test
Null Hypothesis
True
R.Approx.T-Test(T)
False
T.Approx.T-Test(R)
False
Not Normal & Homogeneous ?
True
Mann_Whitney
Null Hypothesis
True
T.Mann_Whitney(R)
False
R.Mann_Whitney(T)
False
Not Normal & Not Homogeneous ?
True
Rankit
$s^2_{R,Rankit} = 0$ & $s^2_{T,Rankit} = 0$?
True
Cannot perform T-Test or Approx T-Test, Exit
False
Move $\bar{y}_R = 0$ $\bar{y}_T = 0$
Levene BioStatWay
StudentT-Test
$s^2_{R,Rankit,\bar{y}=0} = 0$ & $s^2_{T,Rankit,\bar{y}=0} = 0$?
True
StudentsT-Test value=0
False
$s^2_{R,Rankit,\bar{y}=0} = 0$?
True
T.StudentsT-Test(R)
False
Does it mean $s^2_{T,Rankit,\bar{y}=0} = 0$ only OR $s^2_{R,Rankit,\bar{y}=0} \neq 0$ OR both ?
R.StudentsT-Test(T)
Rankit Variable OK ?
True
Null Hypothesis
True
R.StudentsT-Test(T)
False
T.StudentsT-Test(R)
False
Null Hypothesis
True
R.Approx.T-Test(T)
False
T.Approx.T-Test(R)

BIOASSAY STATISTICAL HYPOTHESES

Bioassay Type	Bioassay Endpoint	Null Hypothesis	Alternate Hypothesis
AMP10	MORT	T ≤ R	T > R
BIVLV	ABMO	T ≥ R	T < R
ECHIN	ABMO	T ≥ R	T < R
NEANT	GROW	T ≥ R	T < R
CHR10	GROW	T ≥ C	T < C
CHR10	MORT	T ≤ C	T > C
CHR20	GROW	T ≥ C	T < C
CHR20	MORT	T ≤ C	T > C
HYA10	MORT	T ≤ C	T > C
HYA28	GROW	T ≥ C	T < C
HYA28	MORT	T ≤ C	T > C

Footnote:

AMP10: Amphipod 10 day

BIVLV: Bivalve

ECHIN: Echinoderm

NEANT: Neanthes 20 day

CHR10: Chiromus dilutes 10 day

CHR20: Chiromus dilutes 20 day

HYA10: Hyalella azteca 10 day

HYA28: Hyalella azteca 28 day

MORT: Mortality

ABMO: Abnormality/Mortality, Normal Survivorship

GROW: Growth

T: Test

R: Reference

C: Control

Appendix E: Chemistry Analysis – Updates and Data Aggregation

Suumarized changes for 2014 Spring MyEIM chemistry analysis updates are depicted here. The logic used for data reduction of chemical concentrations using aggregate and maximum rules is discussed here.

SUMMARIZED CHANGES FOR 2014 SPRING MYEIM UPDATES

Some existing cleanup standards have been renamed.

Old Name	New Name
R SMS Marine CSL	R SMS Marine CSL / SIZmax
R SMS Marine SQS	R SMS Marine SQS / SCO
R 1988 Marine CSL Dry	R 1988 Marine CSL / SIZmax Dry
R 1988 Marine SQS Dry	R 1988 Marine SQS / SCO

- The following four chemistry searches replaced two original chemistry searches in the Search Templates:

Name	Description
Chemistry study check	Chemistry study QA
Chemistry sediment data check	Chemistry sediment or soil data QA and analysis per specified source
Chemistry tissue data check	Chemistry tissue data QA and analysis
Chemistry whole specific study data check	Chemistry all sample source data check for specific study

- New cleanup standards for freshwater sediment have been added.

Name	Description
R SMS Freshwater CSL	WA Sediment Management Standards 2013 Freshwater: Cleanup Screening Level
R SMS Freshwater SCO	WA Sediment Management Standards 2013 Freshwater: Sediment Cleanup Objective

- New derived variables in the following table have been added

Name	Description
Total PAHs	Total PAHs
PCB Aroclor Sum	PCB Aroclor Sum
PCB Congener Sum	PCB Congener Sum
Total DDDs	Total DDDs
Total DDEs	Total DDEs
Total DDTs	Total DDTs
CPAH TEQ	Carcinogenic Polycyclic Aromatic Hydrocarbons as TEQ (Cal-EPA 2005
Dioxin-like PCB TEQ	Dioxin like PCB congener TEQ (WHO 2005 TEF)
Dioxin/Furan-TEQ	PCDDs and PCDFs TEQ (WHO 2005 TEF)
Total 2,3,7,8-TCDD TEQ	Total 2,3,7,8-TCDD TEQ (WHO 2005 TEF)

- For existing Marine Sediment and Freshwater Sediment cleanup criteria, the "PCBs" derived variable has been replaced with the new "PCB Aroclor Sum" derived variable.
- Several subsidiaries for derived variables have been added and changed. See the subsidiary section below for a full listing.
- Subsidiaries are now supported for (a) weighted derived variables, provided the weights of the substituted chemicals are equal and (b) user-defined derived variables.
- If cleanup criteria are exceeded, an optional comment (defined in the criteria specification) will be added to the Comments field in the analysis results. Currently, this is only in use by the R SMS Freshwater CSL criteria – "CSL unknown but above the criteria concentration. Bioassays shall be conducted to evaluate potential benthic community toxicity." will appear in the Comments column if certain chemical concentrations are exceeded.
- The following fields have been added to the Chemistry Comparison Results and Derived Variable Results tables.
    - ReportingLimit: Result Reporting Limit value
    - RLType: Result Reporting Limit Type

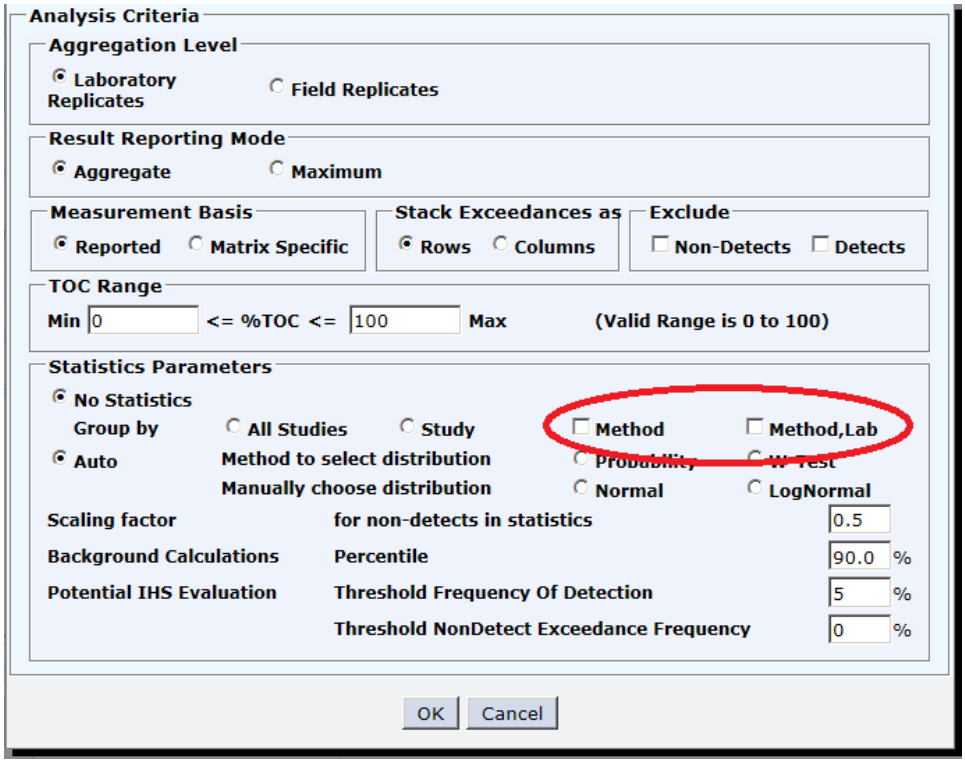
- DetectionLimit: Result Detection Limit value
- DLType: Result Detection Limit Type
- AnalysisMethod: Result Method used by the lab performing the analysis
- AnalysisLab: Result Lab Name, the name of the lab performing the analysis
- ReportedComment: Any comments from the lab performing the analysis.
- ValidationLevel: Result Validation Level specified in the SAP/QAPP and the data validation report. The data validation is done by the third party data experts/validators independent of the lab and the end data users.
- QALevel: Bioassay QA Level Code
- QAPlanning: Study QA Planning Level
- Assessment: Study QA Assessment Level
- Contact: Ecology Contact
- Program: Ecology Program or Other Responsible Entity
- StudyName: Study Name

- The lipid normalized concentration (LipidNormConc) has been added to the Chemistry Comparison Results table for tissue chemistry data analysis
- Several changes have been made to the content of the Comments field in the Chemistry Comparison Results table and Derived Variable Results table; the changes are too numerous to list, but some of the highlights are:
  - For derived variables, the comments field now contains information germane to the individual constituent for example, if a subsidiary is used, the chemicals the subsidiary replaced will be listed.
  - If a derived variable has missing constituents, they will be listed in the comments in the Chemistry Comparison Results table.
- The following fields have been added to the Chemical Statistics table.
  - MinRL: Minimum reporting limit value
  - MaxRL: Maximum reportinlimit value
  - MinDL: Minimum detection limit value
  - MaxDL: Maximum detection limit value
  - AnalysisMethod: The method used by the lab performing the analysis*

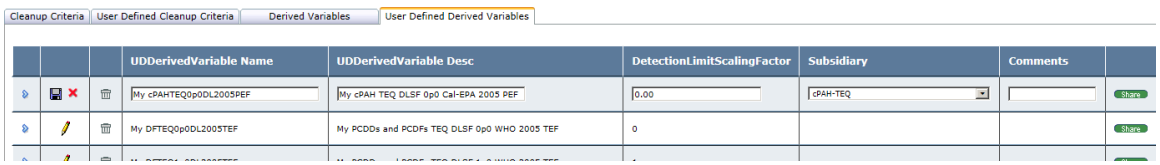
- AnalysisLab: The name of the lab performing the analysis*

  * In order for these to appear, the new checkboxes for Method or Method/Lan on the Chemistry Analysis Preferences must be selected.

- Options “Method” and “Method, Lab” have been added to the Statistics Parameters options for the sediment and MTCA Preferences menu in the analysis standard page. Selecting these will add the “AnalysisMethod” and/or “AnalysisLab” fields to the Statistical Results table for sediment chemistry or MTCA chemistry data analysis.



- The “Subsidiary” column has been added to the User-Defined Derived Variables table. This will determine which subsidiary rules are used for the derived variable (see the Subsidiary Business Rules section below for more details).



Please note that many of the new derived variable business rules will not work with pre-existing user defined derived variables that were created before this release. If you have user-defined derived variables that were copied from system derived variables, it is recommended that you delete and re-copy them, or edit the Subsidiary value as shown above.

DATA REDUCTION AT LABORATORY REPLICATE AND FIELD REPLICATE LEVEL

Data reduction is carried out for sediment data and tissue chemistry data using the same logic with an exception that where necessary sediment data are TOC normalized and tissue data are lipid normalized.

MTCA data reduction is carried out using different logic as detailed at the end. Qualifier code for MTCA data is assigned using the same logic as that for sediment and tissue data.

Sediment and Tissue Data reduction:

For aggregation at laboratory replicate Level, data reduction is carried out for a given chemical in a laboratory replicate collection with unique combination of Study Id

, Study Location Name (EIM field name Study Specific Location ID), Sample Id, iled Collection Start Date (Sample Date), Sample Sub Id and Field Replicate Id. Additonal fields used for uniqueness are Field Collection Upper Depth, Field Collection Lower Depth, Depth Units for sediment and soil data, and sample taxon name and sample tissue type for tissue data.

For Aggregation at field replicate Level, data reduction is carried out for a given chemical in a field replicate collection with unique combination of User Study Id, Study Location Name, Sample Date, Upper Depth, Lower Depth and Depth Unit of Measure. Additonal fields used for uniqueness are Upper Depth, Lower Depth, Depth Unit of Measure for all data except for tissue, where sample taxon name and sample tissue type are used.

Normalize Unit of Measure (UOM) for all values if required:

If the UOM for this chemical reported is different in different replicates.

Convert all the units to the UOM reported in the first replicate.

Report data reduced value:

Using aggregate Rule

If all reported values are detects, take arithmetic mean of detects and report it as the aggregate value.

If reported values contain detects and non-detects, take arithmetic mean of only detect values and report it as the aggregate value.

If all reported values are non-detects, report lowest non-detected value as the aggregate value.

Using maximum Rule

If all are detects or a mix of detects and non-detects, report maximum of detects

If all are non-detects, report maximum of non-detects.

Derived variables data reduction:

After data reduction at lab replicate level, derived variables for each field replicate are calculated using aggregated values of individual constituent chemicals. Therefore the result is always a single value (data reduction NA).

For data reduction at field replicate level, each derived variable is treated in the same as other chemicals.

Report value as aggregated:

If total reported count (number of detected + non-Detected) is > 1, then tag this reported value as Aggregated# = number of replicates used in aggregation.

Qualifier code (QC) assignment:

Using the definitions:

Chemical Is Non Detect if Result Data Qualifier Contains "U" or "B"

Chemical is Estimate if Result Data Qualifier Contains "J"

Using aggregate rule:

If aggregate value is calculated from detects then

If all reported detects QC is the same then report that consistent QC as Result Data Qualifier for the aggregate value.

Otherwise, if any of the detects QC contains "J" then report QC as "J"

Otherwise report QC as empty.

If all reported values are non-detects, report the qualifier code associated with the lowest non-detect value.

If there are more than one same lowest non detect values present, then report qualifier code as "U"

Using maximum rule:

Report qualifier code that goes with the selected maximum value.

TOC normalization

Use arithmetic mean of all TOC values reported with all replicates (having unique combination of User Study ID, Study Location Name, Sample Id, Sample Date,Subsample Id, Field Replicate Id, Upper Depth, Lower Depth, Depth Unit of Measure) and use that value for TOC normalization of the aggregate value.

MTCA Data reduction Logic:

In MyEIM MTCA analysis, criteria comparison and statistics are carried out after data reduction at field replicate level. MTCA data reduction uses the following logic.

If more than one lab replicates are present under each field replicate,

If all reported values are detects or are mixtures of detects and non-detects, then take the maximum value of the detects (even if global maximum is a non detect)

If all reported values are non-detects: Take maximum value of non detects

Using aggregate rule:

If there are more than two field replicates, use the maximum value

If there are two field replicates, then if their ratio is within the range 2/3 and 3/2 (this range is 0.77 to 1.3 for water samples) take arithmetic mean, otherwise take maximum.

Using maximum rule:

If there are more than two field replicates, use the maximum value.

If the constituent chemical UOM is not same as Derived Variable UOM, then UOM normalize the constituent concentration to the UOM of the Derived Variable.

Calculation Bsiness Logics for Simple Derived Variable concentration

If all constituents are detects, then add all detect concentrations and report this sum as the Derived Variable concentration.

If constituents are detects and non-detects, then add all detect concentrations and report this sum as the Derived Variable concentration.

If constituents are non-detects, then report highest non-detect concentration as the Derived Variable concentration.

Qualifier Code assignment:

Using definitions:

Constituent Is Non-Detect if Result Data Qualifier Contains "U" or "B"

Constituent is Estimate if Result Data Qualifier Contains "J"

If aggregate value is calculated from detects then

If all reported detects Qualifier Code is the same then report that consistent Qualifier Code as Qualifier Code for the Derived Variable.

Otherwise, if any of the detects Qualifier Code contains "J" then report Derived Variable Qualifier Code as "J"

Otherwise report Qualifier Code as empty.

If all reported values are non-detects, report the qualifier code associated with the highest non-detect value.

If there are more than one same highest non detect values present, then report qualifier code as "U"

Compute percent contribution for each constituent.

Add comments

If any of the constituents are missing then note "Missing constituents"

If Subsidiary Derived variable value is used, then report as such.

If the "wet" measurement basis is used, then report it.

If TOC normalization required but not possible for any reason then report "Invalid TOC"

Appendix F: Chemistry Analysis – Simple Derived variables

MyEIM logic used for calculation of simple derived variables in chemistry analysis, comparison of simple derived variable to cleanup criteria, and the constituent chemicals of simple derived variables are discussed here.

SIMPLE DERIVED VARIABLES

Derived variable is the chemical derived from a group of chemicals called constituent chemicals. In a simple derived variable, the concentration of constituent chemicals are simply added up to the total value using the subsidiary business rule described below. The simple derived variables implemented for MyEIM chemistry analysis are PCBs, PCB Arocolor Sum, PCB Congener Sum, Total DDDs, Total DDEs, Total DDTs, LPAH. HPAH, Total PAHs, and Percent Fines.

When constituents are absent, use reported derived variable values.

Subsidiary Business Rules

Subsidiaries are replacements for missing constituents of a derived variable. If a subsidiary is used, a comment in the Derived Variable Results table will note which chemicals the subsidiary is replacing. The following describes the subsidiary business logic for all of the new and altered derived variables.

Percent Fines:

- If grain size phi 8-9, 9-10, and 10-infinity are not present, use Total Percent Clay.
- If grain size phi 4-5, 5-6, 6-7, and 7-8 are not present, use Total Percent Silt.
- If all phi scale are not present, use Total Percent Fines.

PCBs:

- If Aroclor -1016 and Aroclor-1242 are not present, use Aroclor -1016/1242.
- If Aroclor -1254 and Aroclor -1260 are not present, use Aroclor -1254/1260.
- If all constituents are not present,
    - Use PCB, Sum of Aroclors.
    - If PCB, Sum of Aroclors are not present, use PCB (CAS 1336-36-3).
    - If PCB (CAS 1336-36-3) is not present, use PCB, Sum of Congeners.

Total Benzofluoranthenes:

- If Benzo(b)fluoranthene and Benzo(k)fluoranthene are not present, use Benzo(b,k)fluoranthene.
- If Benzo(b,k)fluoranthene is not present, use Benzo(b,j,k)fluoranthene.

LPAH:

- If none of the constituents are present, use LPAH.

HPAH:

- If Benzo(b)fluoranthene and Benzo(k)fluoranthene are not present, use Benzo(b,k)fluoranthene.
- If Benzo(b,k)fluoranthene is not present, use Benzo(b,j,k)fluoranthene.
- If Benzo(b,j,k)fluoranthene is not present, use Benzofluoranthene.
- If Benzo(j)fluoranthene and Benzo(k)fluoranthene are not present, use Benzo(j,k)fluoranthene.
- If none of the constituents are present, use HPAH.

Total DDDs:

- If none of the constituents are present, use Total DDDs.

Total DDEs:

- If none of the constituents are present, use Total DDEs.

Total DDTs:

- If none of the constituents are present, use Total DDTs.

Total PAH:

- If Benzo(b)fluoranthene and Benzo(k)fluoranthene are not present, use Benzo(b,k)fluoranthene.
- If Benzo(b,k)fluoranthene is not present, use Benzo(b,j,k)fluoranthene.
- If Benzo(b,j,k)fluoranthene is not present, use Benzofluoranthene.
- If Benzo(j)fluoranthene and Benzo(k)fluoranthene are not present, use Benzo(j,k)fluoranthene.
- If none of the constituents are present, use Total PAHs.

PCDDs and PCDFs TEQ:

- If none of the constituents are present, use dioxins and furans as 2,3,7,8-tcdd teqs

Dioxin-like PCB TEQ and Total 2,3,7,8-TCDD TEQ:

- If PCB-105 is not present, use PCB-105/127. A note will be made in the Comments column in the Chemistry Analysis results table because the concentration is an overestimate.
- If PCB-156 and PCB-157 are not present, use PCB-156/157.
- If PCB-156 is not present, use PCB-156/171/202. A note will be made in the Comments column in the Chemistry Analysis results table because the concentration is an overestimate.
- If PCB-077 is not present, use PCB-077/110. A note will be made in the Comments column in the Chemistry Analysis results table because the concentration is an overestimate.
- If PCB-123 is not present, use PCB-123/149. A note will be made in the Comments column in the Chemistry Analysis results table because the concentration is an overestimate.
- If PCB-123 and PCB-123/149 are not present, use PCB-123/153. A note will be made in the Comments column in the Chemistry Analysis results table because the concentration is an overestimate.
- If PCB-118 is not present, use PCB-106/118. A note will be made in the Comments column in the Chemistry Analysis results table because the concentration is an overestimate.
- For Total 2,3,7,8-TCDD TEQ, a note will be made in the Comments column in the Chemistry Analysis results indicating the relative contribution of Dioxin-like PCB TEQ and Dioxin/Furan-TEQ. If one of these groups is completely missing, the derived variable will not show up in the results.

PCB Aroclor Sum:

- If Aroclor -1016 and Aroclor-1242 are not present, use Aroclor -1016/1242.
- If Aroclor -1254 and Aroclor -1260 are not present, use Aroclor -1254/1260.
- If none of the constituents are present, use PCB, Sum of Aroclors and add the comment "Reported as PCB, Sum of Aroclors". Otherwise, add the comment "Derived as PCB Aroclor Sum".
- If PCB, Sum of Aroclors is not present, use PCB (CAS 1336-36-3); add the comment "Reported as PCB (CAS 1336-36-3)".
- If PCB (CAS 1336-36-3) is not present, use the subsidiary logic for PCB Congener Sum (see below).

PCB Congener Sum:

- If PCB-004 and PCB-010 are not present, use PCB-004/010.
- If PCB-005 and PCB-008 are not present, use PCB-005/008.
- If PCB-007 and PCB-009 are not present, use PCB-007/009.
- If PCB-012 and PCB-013 are not present, use PCB-012/013.
- If PCB-016 and PCB-032 are not present, use PCB-016/032.
- If PCB-018 and PCB-030 are not present, use PCB-018/030.
- If PCB-020 and PCB-021 and PCB-033 are not present, use PCB-020/021/033.
- If PCB-020 and PCB-028 are not present, use PCB-020/028.
- If PCB-020 and PCB-033 are not present, use PCB-020/033.

- If PCB-021 and PCB-033 are not present, use PCB-021/033.
- If PCB-023 and PCB-034 are not present, use PCB-023/034.
- If PCB-024 and PCB-027 are not present, use PCB-024/027.
- If PCB-026 and PCB-029 are not present, use PCB-026/029.
- If PCB-028 and PCB-031 are not present, use PCB-028/031.
- If PCB-040 and PCB-057 are not present, use PCB-040/057.
- If PCB-040 and PCB-071 are not present, use PCB-040/071.
- If PCB-040 and PCB-041 and PCB-071 are not present, use PCB-040/041/071.
- If PCB-041 and PCB-071 and PCB-072 are not present, use PCB-041/071/072.
- If PCB-041 and PCB-064 and PCB-068 are not present, use PCB-041/064/068.
- If PCB-041 and PCB-064 and PCB-071 are not present, use PCB-041/064/071.
- If PCB-041 and PCB-068 are not present, use PCB-041/068.
- If PCB-042 and PCB-051 are not present, use PCB-042/051.
- If PCB-042 and PCB-059 are not present, use PCB-042/059.
- If PCB-043 and PCB-049 are not present, use PCB-043/049.
- If PCB-043 and PCB-073 are not present, use PCB-043/073.
- If PCB-044 and PCB-047 and PCB-065 are not present, use PCB-044/047/065.
- If PCB-045 and PCB-051 are not present, use PCB-045/051.
- If PCB-046 and PCB-049 are not present, use PCB-046/049.
- If PCB-046 and PCB-069 and PCB-073 are not present, use PCB-046/069/073.
- If PCB-047 and PCB-048 and PCB-075 are not present, use PCB-047/048/075.
- If PCB-047 and PCB-062 and PCB-075 are not present, use PCB-047/062/075.
- If PCB-047 and PCB-048 are not present, use PCB-047/048.
- If PCB-048 and PCB-075 are not present, use PCB-048/075.
- If PCB-049 and PCB-069 are not present, use PCB-049/069.
- If PCB-050 and PCB-053 are not present, use PCB-050/053.
- If PCB-052 and PCB-069 are not present, use PCB-052/069.
- If PCB-052 and PCB-073 are not present, use PCB-052/073.
- If PCB-055 and PCB-080 are not present, use PCB-055/080.
- If PCB-056 and PCB-060 are not present, use PCB-056/060.
- If PCB-059 and PCB-062 and PCB-075 are not present, use PCB-059/062/075.
- If PCB-061 and PCB-070 are not present, use PCB-061/070.
- If PCB-061 and PCB-070 and PCB-074 and PCB-076 are not present, use PCB-061/070/074/076.
- If PCB-061 and PCB-074 are not present, use PCB-061/074.
- If PCB-064 and PCB-068 are not present, use PCB-064/068.
- If PCB-064 and PCB-072 are not present, use PCB-064/072.
- If PCB-065 and PCB-075 are not present, use PCB-065/075.

- If PCB-066 and PCB-076 are not present, use PCB-066/076.
- If PCB-066 and PCB-076 and PCB-080 are not present, use PCB-066/076/080.
- If PCB-066 and PCB-080 are not present, use PCB-066/080.
- If PCB-069 and PCB-073 are not present, use PCB-069/073.
- If PCB-071 and PCB-072 are not present, use PCB-071/072.
- If PCB-077 and PCB-110 are not present, use PCB-077/110.
- If PCB-082 and PCB-120 are not present, use PCB-082/120.
- If PCB-083 and PCB-109 are not present, use PCB-083/109.
- If PCB-083 and PCB-099 are not present, use PCB-083/099.
- If PCB-083 and PCB-108 are not present, use PCB-083/108.
- If PCB-084 and PCB-092 are not present, use PCB-084/092.
- If PCB-085 and PCB-124 are not present, use PCB-085/124.
- If PCB-085 and PCB-116 are not present, use PCB-085/116.
- If PCB-085 and PCB-116 and PCB-117 are not present, use PCB-085/116/117.
- If PCB-085 and PCB-120 are not present, use PCB-085/120.
- If PCB-086 and PCB-087 and PCB-097 and PCB-111 and PCB-117 and PCB-125 are not present, use PCB-086/087/097/111/117/125
- If PCB-086 and PCB-116 and PCB-117 are not present, use PCB-086/116/117.
- If PCB-086 and PCB-087 and PCB-097 and PCB-108 and PCB-119 and PCB-125 are not present, use PCB-086/087/097/108/119/125
- If PCB-086 and PCB-087 and PCB-097 and PCB-111 and PCB-125 are not present, use PCB-086/087/097/111/125
- If PCB-086 and PCB-117 are not present, use PCB-086/117.
- If PCB-086 and PCB-087 and PCB-097 and PCB-109 and PCB-119 and PCB-125 are not present, use PCB-086/087/097/109/119/125
- If PCB-086 and PCB-097 and PCB-117 are not present, use PCB-086/097/117.
- If PCB-086 and PCB-087 and PCB-097 and PCB-111 and PCB-115 and PCB-116 and PCB-117 and PCB-125 are not present, use PCB-086/087/097/111/115/116/117/125
- If PCB-086 and PCB-097 and PCB-125 are not present, use PCB-086/097/125.
- If PCB-087 and PCB-111 are not present, use PCB-087/111.
- If PCB-087 and PCB-115 are not present, use PCB-087/115.
- If PCB-087 and PCB-117 and PCB-125 are not present, use PCB-087/117/125.
- If PCB-088 and PCB-091 are not present, use PCB-088/091.
- If PCB-088 and PCB-121 are not present, use PCB-088/121.
- If PCB-089 and PCB-101 and PCB-113 are not present, use PCB-089/101/113.
- If PCB-089 and PCB-090 are not present, use PCB-089/090.
- If PCB-089 and PCB-090 and PCB-101 are not present, use PCB-089/090/101.
- If PCB-089 and PCB-101 are not present, use PCB-089/101.

- If PCB-090 and PCB-101 are not present, use PCB-090/101.
- If PCB-090 and PCB-101 and PCB-113 are not present, use PCB-090/101/113.
- If PCB-091 and PCB-121 are not present, use PCB-091/121.
- If PCB-093 and PCB-095 and PCB-098 and PCB-100 and PCB-102 are not present, use PCB-093/095/099/100/102.
- If PCB-093 and PCB-098 and PCB-102 are not present, use PCB-093/098/102.
- If PCB-093 and PCB-095 and PCB-098 and PCB-102 are not present, use PCB-093/095/098/102.
- If PCB-093 and PCB-100 are not present, use PCB-093/100.
- If PCB-093 and PCB-095 and PCB-121 are not present, use PCB-093/095/121.
- If PCB-093 and PCB-102 are not present, use PCB-093/102.
- If PCB-093 and PCB-098 and PCB-100 and PCB-102 are not present, use PCB-093/098/100/102.
- If PCB-093 and PCB-095 are not present, use PCB-093/095.
- If PCB-095 and PCB-121 are not present, use PCB-095/121.
- If PCB-095 and PCB-098 are not present, use PCB-095/098.
- If PCB-095 and PCB-098 and PCB-102 are not present, use PCB-095/098/102.
- If PCB-097 and PCB-116 are not present, use PCB-097/116.
- If PCB-097 and PCB-125 are not present, use PCB-097/125.
- If PCB-098 and PCB-102 are not present, use PCB-098/102.
- If PCB-101 and PCB-090 are not present, use PCB-101/090.
- If PCB-105 and PCB-127 are not present, use PCB-105/127.
- If PCB-106 and PCB-118 are not present, use PCB-106/118.
- If PCB-107 and PCB-108 are not present, use PCB-107/108.
- If PCB-107 and PCB-109 are not present, use PCB-107/109.
- If PCB-107 and PCB-124 are not present, use PCB-107/124.
- If PCB-108 and PCB-112 are not present, use PCB-108/112.
- If PCB-108 and PCB-124 are not present, use PCB-108/124.
- If PCB-110 and PCB-115 are not present, use PCB-110/115.
- If PCB-110 and PCB-120 are not present, use PCB-110/120.
- If PCB-111 and PCB-116 and PCB-117 are not present, use PCB-111/116/117.
- If PCB-111 and PCB-115 are not present, use PCB-111/115.
- If PCB-112 and PCB-119 are not present, use PCB-112/119.
- If PCB-115 and PCB-116 are not present, use PCB-115/116.
- If PCB-116 and PCB-125 are not present, use PCB-116/125.
- If PCB-123 and PCB-153 are not present, use PCB-123/153.
- If PCB-123 and PCB-149 are not present, use PCB-123/149.
- If PCB-128 and PCB-162 are not present, use PCB-128/162.
- If PCB-128 and PCB-166 are not present, use PCB-128/166.

- If PCB-128 and PCB-167 are not present, use PCB-128/167.
- If PCB-129 and PCB-138 and PCB-163 are not present, use PCB-129/138/163.
- If PCB-129 and PCB-138 and PCB-160 and PCB-163 are not present, use PCB-129/138/160/163.
- If PCB-131 and PCB-133 are not present, use PCB-131/133.
- If PCB-131 and PCB-142 and PCB-165 are not present, use PCB-131/142/165.
- If PCB-132 and PCB-153 and PCB-160 are not present, use PCB-132/153/160.
- If PCB-132 and PCB-153 and PCB-168 are not present, use PCB-132/153/168.
- If PCB-132 and PCB-161 are not present, use PCB-132/161.
- If PCB-132 and PCB-146 are not present, use PCB-132/146.
- If PCB-132 and PCB-168 are not present, use PCB-132/168.
- If PCB-132 and PCB-153 are not present, use PCB-132/153.
- If PCB-133 and PCB-142 are not present, use PCB-133/142.
- If PCB-134 and PCB-143 are not present, use PCB-134/143.
- If PCB-135 and PCB-144 are not present, use PCB-135/144.
- If PCB-135 and PCB-151 are not present, use PCB-135/151.
- If PCB-135 and PCB-151 and PCB-154 are not present, use PCB-135/151/154.
- If PCB-136 and PCB-148 are not present, use PCB-136/148.
- If PCB-138 and PCB-160 are not present, use PCB-138/160.
- If PCB-138 and PCB-163 are not present, use PCB-138/163.
- If PCB-138 and PCB-163 and PCB-164 are not present, use PCB-138/163/164.
- If PCB-139 and PCB-140 are not present, use PCB-139/140.
- If PCB-139 and PCB-149 are not present, use PCB-139/149.
- If PCB-141 and PCB-179 are not present, use PCB-141/179.
- If PCB-146 and PCB-161 are not present, use PCB-146/161.
- If PCB-146 and PCB-165 are not present, use PCB-146/165.
- If PCB-147 and PCB-149 are not present, use PCB-147/149.
- If PCB-153 and PCB-173 and PCB-201 are not present, use PCB-153/173/201.
- If PCB-153 and PCB-168 are not present, use PCB-153/168.
- If PCB-156 and PCB-157 are not present, use PCB-156/157.
- If PCB-156 and PCB-171 and PCB-202 are not present, use PCB-156/171/202.
- If PCB-158 and PCB-160 are not present, use PCB-158/160.
- If PCB-163 and PCB-164 are not present, use PCB-163/164.
- If PCB-170 and PCB-190 are not present, use PCB-170/190.
- If PCB-171 and PCB-173 are not present, use PCB-171/173.
- If PCB-171 and PCB-202 are not present, use PCB-171/202.
- If PCB-172 and PCB-192 are not present, use PCB-172/192.
- If PCB-172 and PCB-197 are not present, use PCB-172/197.

- If PCB-180 and PCB-193 are not present, use PCB-180/193.
- If PCB-182 and PCB-187 are not present, use PCB-182/187.
- If PCB-183 and PCB-185 are not present, use PCB-183/185.
- If PCB-187 and PCB-159 and PCB-182 are not present, use PCB-187/159/182.
- If PCB-195 and PCB-208 are not present, use PCB-195/208.
- If PCB-196 and PCB-203 are not present, use PCB-196/203.
- If PCB-197 and PCB-200 are not present, use PCB-197/200.
- If PCB-198 and PCB-199 are not present, use PCB-198/199.
- If none of the constituents are present, use PCB, Sum of Congeners and add the comment "Reported as PCB, Sum of Congeners".
  Otherwise, add the comment "Derived as PCB Congener Sum".

PCBs

If constituents of PCB-aroclor 1016 and PCB-aroclor 1242 are absent, then use PCB-aroclor 1016/1242 if reported

If constituents of PCB-aroclor 1254 and PCB-aroclor 1260 are absent, then use PCB-aroclor 1254/1260 if reported

If all constituents of PCB are absent, then use PCB Sum of Aroclors if reported

If all constituents of PCB and PCB Sum of Aroclors are absent, then use PCB_CAS_1336-36-3 if reported

PCB Aroclor Sum

1. If PCB Aroclor Sum can be calculated by MYEIM, compare MyEIM calculated PCB Aroclor sum to Total PCBs or Total PCB Aroclors.
2. If PCB Aroclors cannot be calculated from Step 1, find reported PCB, Sum of Aroclors to compare to Total PCBs or Total PCB Aroclors.
3. If PCB Aroclor Sum cannot be calculated from Step 1, and reported PCB, Sum of Aroclors from step 2 cannot be found, find reported PCB (CAS Number 1336-36-3) to Total PCBs or Total PCB Aroclors.
4. If PCB Aroclors cannot be calculated from Step 1, reported PCB, Sum of Aroclors from step 2, and reported PCB (CAS Number 1336-36-3) from step 3 cannot be found, compare MyEIM calculated PCB Congener Sum to Total PCBs or Total PCB Aroclors.
5. If PCB Aroclors cannot be calculated byMyEIM from Step 1, and reported PCB, Sum of Aroclors from step 2 and reported PCB (CAS Number 1336-36-3) from step 3 cannot be found, and PCB Congener Sum cannot be calculated by MyEIM from step 4, find reported PCB, Sum of Congeners to compare to Total PCBs or Total PCB Aroclors.

PCB Congener Sum

Business logic for PCB Aroclor Sum / PCB Congener Sum comparison to PCBs and Total PCB Aroclors in SMS criteria:

1. If PCB Aroclor sum can be calculated by MYEIM, compare MyEIM calculated PCB Aroclor sum to Total PCBs or Total PCB Aroclors.
2. If PCB Aroclors cannot be calculated from Step 1, find reported PCB, sum of Aroclors to compare to Total PCBs or Total PCB Aroclors.
3. If PCB Aroclors cannot be calculated from Step 1, and PCB, sum of Aroclors from step 2 cannot be found, compare MyEIM calculated PCB congener sum to Total PCBs or Total PCB Aroclors.
4. If PCB Aroclors cannot be calculated byMyEIM from Step 1, and reported PCB, sum of Aroclors from step 2 cannot be found, and PCB congener sum cannot be calculated by MyEIM from step 3, find reported PCB, sum of congeners to compare to Total PCBs or Total PCB Aroclors.
5. If PCB Aroclors cannot be calculated by MyEIM from Step 1, and reported PCB, sum of Aroclors from step 2 cannot be found, and PCB congener sum cannot be calculated by MyEIM from step 3, find reported PCB, sum of congeners to compare to Total PCBs or Total PCB Aroclors.
6. If PCB Aroclors cannot be calculated by MyEIM from Step 1, reported PCB, sum of Aroclors from step 2 cannot be found, PCB congener sum cannot be calculated by MyEIM from step 3, and reported PCB, sum of congeners from step 4 cannot be found, find PCB (CAS Number 1336-36-3) to compare to Total PCBs or Total PCB Aroclors.

Nomalization of Measurement Basis (Result Basis) and UOM (Result Unit) for each constituent chemical to the same ones for derived variable:

Measurement Basis of the Derived Variable is same as that of constituent chemical then use the constituent's aggregate value.

If Derived Variable measurement basis is "dry" (or "wet", see the note below) and constituent chemical Measurement Basis is "dry" (or "wet", see the note below) then use the constituent's aggregate value.

If Derived Variable measurement basis is "toc" and constituent chemical Measurement Basis is "dry" (or "wet", see the note below) then use constituent's TOC Normalized value;

Note: Treat measurement basis "wet" as "dry" only for the sample source of "brackish" "freshwater sediment" or "salt/marine sediment"

UOM Normalization For each constituent chemical:

If the constituent chemical UOM is not same as Derived Variable UOM, then UOM normalize the constituent concentration to the UOM of the Derived Variable.

Calculation Bsiness Logics for Simple Derived Variable concentration

If all constituents are detects, then add all detect concentrations and report this sum as the Derived Variable concentration.

If constituents are detects and non-detects, then add all detect concentrations and report this sum as the Derived Variable concentration.

If constituents are non-detects, then report highest non-detect concentration as the Derived Variable concentration.

Qualifier Code assignment:

Using definitions:

Constituent Is Non-Detect if Result Data Qualifier Contains "U" or "B"

Constituent is Estimate if Result Data Qualifier Contains "J"

If aggregate value is calculated from detects then

If all reported detects Qualifier Code is the same then report that consistent Qualifier Code as Qualifier Code for the Derived Variable.

Otherwise, if any of the detects Qualifier Code contains "J" then report Derived Variable Qualifier Code as "J"

Otherwise report Qualifier Code as empty.

If all reported values are non-detects, report the qualifier code associated with the highest non-detect value.

If there are more than one same highest non detect values present, then report qualifier code as "U"

Compute percent contribution for each constituent.

Add comments

If any of the constituents are missing then note "Missing constituents"

If Subsidiary Derived variable value is used, then report as such.

If the "wet" measurement basis is used, then report it.

If TOC normalization required but not possible for any reason then report "Invalid TOC"

Appendix G: Chemistry Analysis – Weighted Derived Variables

MyEIM logic used for calculation of weighted derived variables in chemistry analysis is discussed here.

WEIGHTED DERIVED VARIABLES

In a weighted derived variable, concentrations of constituent chemicals are weighted using the TEQ factors and then added up to the total value using the logic discussed here. For this reason these derived variables are also called TEQ derived variables. A detection limit scaling factor is used to further scale down the non-detect concentrations.

When constituents are absent, use reported derived variable values.

Subsidiary Business Rules

Subsidiaries are replacements for missing constituents of a derived variable. If a subsidiary is used, a comment in the Derived Variable Results table will note which chemicals the subsidiary is replacing. The following describes the subsidiary business logic for all of the new and altered derived variables.

cPAH-TEQ:

- If Benzo(b)fluoranthene and Benzo(k)fluoranthene are not present, use Benzo(b,k)fluoranthene.
- If Benzo(b,k)fluoranthene is not present, use Benzo(b,j,k)fluoranthene.
- If Benzo(b,j,k)fluoranthene is not present, use Benzofluoranthene.
- If Benzo(j)fluoranthene and Benzo(k)fluoranthene are not present, use Benzo(j,k)fluoranthene.
- If none of the constituents are present, use cPAH-TEQ.

PCDDs and PCDFs TEQ:

- If none of the constituents are present, use dioxins and furans as 2,3,7,8-tcdd teqs

Dioxin-like PCB TEQ and Total 2,3,7,8-TCDD TEQ:

- If PCB-105 is not present, use PCB-105/127. A note will be made in the Comments column in the Chemistry Analysis results table because the concentration is an overestimate.
- If PCB-156 and PCB-157 are not present, use PCB-156/157.
- If PCB-156 is not present, use PCB-156/171/202. A note will be made in the Comments column in the Chemistry Analysis results table because the concentration is an overestimate.
- If PCB-077 is not present, use PCB-077/110. A note will be made in the Comments column in the Chemistry Analysis results table because the concentration is an overestimate.
- If PCB-123 is not present, use PCB-123/149. A note will be made in the Comments column in the Chemistry Analysis results table because the concentration is an overestimate.
- If PCB-123 and PCB-123/149 are not present, use PCB-123/153. A note will be made in the Comments column in the Chemistry Analysis results table because the concentration is an overestimate.
- If PCB-118 is not present, use PCB-106/118. A note will be made in the Comments column in the Chemistry Analysis results table because the concentration is an overestimate.
- For Total 2,3,7,8-TCDD TEQ, a note will be made in the Comments column in the Chemistry Analysis results indicating the relative contribution of Dioxin-like PCB TEQ and Dioxin/Furan-TEQ. If one of these groups is completely missing, the derived variable will not show up in the results.

Measurement Basis Normalization For each constituent chemical:

If Measurement Basis of the Derived Variable criteria is the same as that of constituent chemical then use the constituent's aggregate value.

If Derived Variable criteria measurement basis is "toc" and constituent chemical Measurement Basis is "dry", then use TOC Normalized value.

Treat measurement basis "wet"* and blank as "dry" only for the sample source of "brackish" "freshwater sediment" or "salt/marine sediment", when Matrix Specific measurement basis in the Preference menu is chosen.

Treat measurement basis "dry"* and blank as "wet" only for the sample source of "animal tissue" ", when Matrix Specific measurement basis in the Preference menu is chosen.

UOM Normalization For each constituent chemical:

If the constituent chemical UOM is not same as Derived Variable UOM, then UOM normalize the constituent concentration to the UOM of the Derived Variable.

Calculate Derived Variable concentration

Scale each constituent concentration by the TEF factor (weight).

If the constituent is a non-detect then scale the resulting concentration with the DLSF factor.

Sum all resulting concentrations to get the Derived Variable concentration.

Qualifier Code assignment:

Using the definitions:

Constituent Is Non-Detect if Result Data Qualifier Contains "U" or "B"

Constituent is Estimate if Result Data Qualifier Contains "J"

If all constituent QC is the same, then report that consistent QC as Qualifier for the Derived Variable.

Otherwise, if any of the constituents QC contains "J" then report QC as "J"

If all reported values are non-detects and reported non-detects Qualifier Codes are the same then report that consistent Qualifier Code as Derived Variable Qualifier Code.

If all reported values are non-detects with different Qualifier Codes, report the qualifier code "U" (it does not matter if there are more than one constituent with the same value)

Otherwise report Qualifier Code as empty.

Compute percent contribution for each constituent.

Add comments

If any of the constituents are missing then note "Missing constituents"

If the "wet" or "dry" measurement basis is used, then report it.

If TOC normalization required but not possible then report "Invalid TOC"

Appendix H: PIHS decision tree

This flow diagram depicts the decision tree for identifying potential indicator hazardous substances (PIHS) based on the concentration data and criteria value.

PIHS LOGIC

Decision Box: 

Process Box: 

Potential IHS Box: 

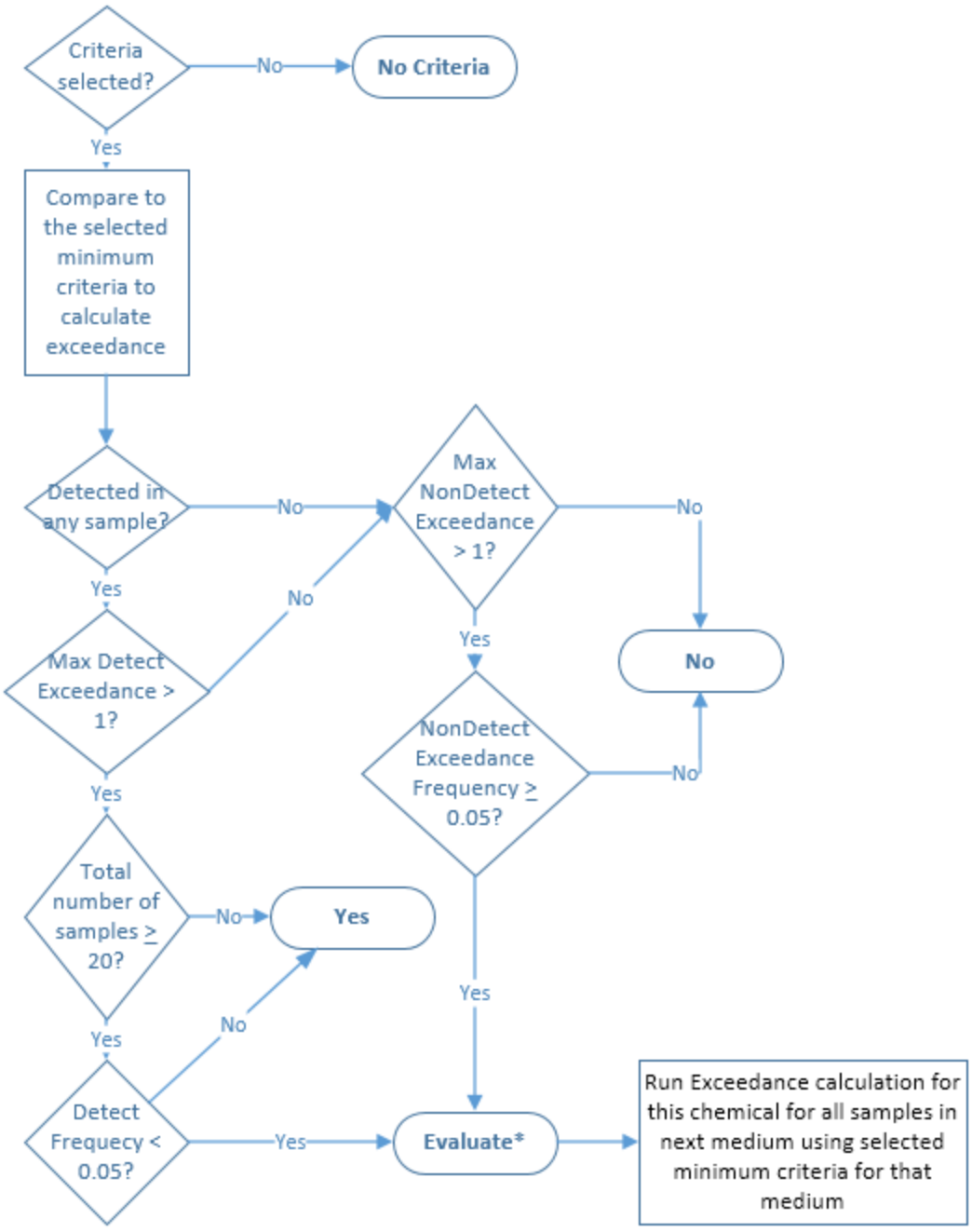
Evaluate*:

Identification of this chemical as an IHS is contingent upon its Exceedance in the next medium along the pollutant propagation path.

The next medium is found in the hierarchy: Soil > ground water> fresh water > sediment.

"Chemicals known to be site-related or that cluster in specific areas of the harbor (indicating a potential hotspot) will be evaluated further.

Note: MyEIM cannot run calculations for two media side by side under current architecture. User will run MyEIM for analyzing samples in the next medium and manually combine the results to identify PIHSs.


Criteria selected?
No
No Criteria
Yes
Compare to the selected minimum criteria to calculate exceedance
Detected in any sample?
No
Max NonDetect Exceedance > 1?
No
Yes
No
Max Detect Exceedance > 1?
No
Yes
No
NonDetect Exceedance Frequency ≥ 0.05?
No
Yes
Total number of samples ≥ 20?
No
Yes
Yes
No
Detect Frequecy < 0.05?
Yes
Evaluate*
Run Exceedance calculation for this chemical for all samples in next medium using selected minimum criteria for that medium

IDENTIFY PIHS EXAMPLES

You can identify the potential indicator hazardous substances for the specified sample source on the statistical summary spreadsheet, when all the cleanup site data of your interest for the specified sample source of interest are in EIM, searched and compared to the appropriately selected cleanup criteria (risk based concentration or PQL or natural background per MTCA/SMS cleanup criteria selection hierarchy)

Select 'Yes' in 'Potential_IHS'. Select 'Sort Largest to Smallest' in 'FreqOfDetect_Exceedance' or 'MaxDetect_Exceedance' fields on the statistical summary spreadsheet to identify all potential indicator substances and the major risk drivers for each sample source as shown in Figures 1a and 1b for marine sediment, and Figures 1c and 1d for soil

ChemicalName	MeasurementBas	Criteria_Name	MinCriteriaValu	MaxDetect_Exceedance	MaxNonDetect_Exceedance	FreqOfDetectio	FreqOfDetect_Exceedanc	FreqOfNonDetect_Exceedance	Potential_IHS
fluoranthene	dry	R 1988 Marine SQS / SCO Dry	1700	70.59		1	0.25		Yes
chrysene	dry	R 1988 Marine SQS / SCO Dry	1400	21.43		1	0.22		Yes
copper	dry	R 1988 Marine SQS / SCO Dry	390	11.44		1	0.2045		Yes
dimethyl phthalate	dry	R 1988 Marine SQS / SCO Dry	71	115.5	4.507	0.3673	0.2041	0.04082	Yes
fluoranthene	toc	R SMS Marine SQS / SCO	160	37.5		1	0.1875		Yes
total pcbs	dry	R 1988 Marine SQS / SCO Dry	130	98.46	0.03077	0.6818	0.1818		Yes
pyrene	dry	R 1988 Marine SQS / SCO Dry	2600	29.62		1	0.1702		Yes
mercury	dry	R 1988 Marine SQS / SCO Dry	0.41	10.46	0.122	0.9811	0.1698		Yes
bis(2-ethylhexyl) phthalate	dry	R 1988 Marine SQS / SCO Dry	1300	92.31	0.2462	0.898	0.1633		Yes
bis(2-ethylhexyl) phthalate	toc	R SMS Marine SQS / SCO	47	32.48	0.006809	0.898	0.1633		Yes
total pcbs	toc	R SMS Marine SQS / SCO	12	55.77	0.084	0.6818	0.1591		Yes
zinc	dry	R 1988 Marine SQS / SCO Dry	410	4.829		1	0.1591		Yes
total benzofluoranthenes	dry	R 1988 Marine SQS / SCO Dry	3200	3.125	0.00625	0.9796	0.1429		Yes
hpah	dry	R 1988 Marine SQS / SCO Dry	12000	20.22		1	0.14		Yes
chrysene	toc	R SMS Marine SQS / SCO	110	13.64		1	0.14		Yes
benz(a)anthracene	dry	R 1988 Marine SQS / SCO Dry	1300	2.154		1	0.1333		Yes
butyl benzyl phthalate	dry	R 1988 Marine SQS / SCO Dry	63	13.81	5.079	0.2083	0.125	0.04167	Yes
hpah	toc	R SMS Marine SQS / SCO	960	12.64		1	0.12		Yes
dibenzo(a,h)anthracene	toc	R SMS Marine SQS / SCO	12	2.743	0.008333	0.8333	0.119		Yes
dibenzo(a,h)anthracene	dry	R 1988 Marine SQS / SCO Dry	230	2.609	0.4348	0.8333	0.119		Yes
arsenic	dry	R 1988 Marine SQS / SCO Dry	57	4.211	0.1754	0.5909	0.1136		Yes
acenaphthene	toc	R SMS Marine SQS / SCO	16	13.36	0.00125	0.8667	0.1111		Yes
phenanthrene	dry	R 1988 Marine SQS / SCO Dry	1500	73.33		1	0.1087		Yes
butyl benzyl phthalate	toc	R SMS Marine SQS / SCO	4.9	9.024	0.06531	0.2083	0.1042		Yes
indeno(1,2,3-c,d)pyrene	dry	R 1988 Marine SQS / SCO Dry	600	2.167	0.1667	0.925	0.1		Yes

Figure 1a – Identify AODE5271 RI Sediment PIHS Selecting 'Sort Largest to Smallest' in 'FreqOfDetect_Exceedance'

ChemicalName	MeasurementBas	Criteria_Name	MinCriteriaValu	MaxDetect_Exceedance	MaxNonDetect_Exceedance	FreqOfDetectio	FreqOfDetect_Exceedanc	FreqOfNonDetect_Exceedance	Potential_IHS
benzyl alcohol	dry	R 1988 Marine SQS / SCO Dry	57	228.1	9.123	0.1042	0.08333	0.125	Yes
dimethyl phthalate	dry	R 1988 Marine SQS / SCO Dry	71	115.5	4.507	0.3673	0.2041	0.04082	Yes
total pcbs	dry	R 1988 Marine SQS / SCO Dry	130	98.46	0.03077	0.6818	0.1818		Yes
bis(2-ethylhexyl) phthalate	dry	R 1988 Marine SQS / SCO Dry	1300	92.31	0.2462	0.898	0.1633		Yes
phenanthrene	dry	R 1988 Marine SQS / SCO Dry	1500	73.33		1	0.1087		Yes
fluoranthene	dry	R 1988 Marine SQS / SCO Dry	1700	70.59		1	0.25		Yes
total pcbs	toc	R SMS Marine SQS / SCO	12	55.77	0.084	0.6818	0.1591		Yes
phenanthrene	toc	R SMS Marine SQS / SCO	100	55		1	0.06522		Yes
fluoranthene	toc	R SMS Marine SQS / SCO	160	37.5		1	0.1875		Yes
bis(2-ethylhexyl) phthalate	toc	R SMS Marine SQS / SCO	47	32.48	0.006809	0.898	0.1633		Yes
pyrene	dry	R 1988 Marine SQS / SCO Dry	2600	29.62		1	0.1702		Yes
chrysene	dry	R 1988 Marine SQS / SCO Dry	1400	21.43		1	0.22		Yes
lpah	dry	R 1988 Marine SQS / SCO Dry	5200	21.41		1	0.02		Yes
hpah	dry	R 1988 Marine SQS / SCO Dry	12000	20.22		1	0.14		Yes
lpah	toc	R SMS Marine SQS / SCO	370	15.05		1	0.02		Yes
butyl benzyl phthalate	dry	R 1988 Marine SQS / SCO Dry	63	13.81	5.079	0.2083	0.125	0.04167	Yes
chrysene	toc	R SMS Marine SQS / SCO	110	13.64		1	0.14		Yes
acenaphthene	toc	R SMS Marine SQS / SCO	16	13.36	0.00125	0.8667	0.1111		Yes
hpah	toc	R SMS Marine SQS / SCO	960	12.64		1	0.12		Yes
copper	dry	R 1988 Marine SQS / SCO Dry	390	11.44		1	0.2045		Yes
mercury	dry	R 1988 Marine SQS / SCO Dry	0.41	10.46	0.122	0.9811	0.1698		Yes
butyl benzyl phthalate	toc	R SMS Marine SQS / SCO	4.9	9.024	0.06531	0.2083	0.1042		Yes
acenaphthene	dry	R 1988 Marine SQS / SCO Dry	500	6.2	0.04	0.8667	0.02222		Yes
benz(a)anthracene	toc	R SMS Marine SQS / SCO	110	5.955		1	0.04444		Yes
zinc	dry	R 1988 Marine SQS / SCO Dry	410	4.829		1	0.1591		Yes
arsenic	dry	R 1988 Marine SQS / SCO Dry	57	4.211	0.1754	0.5909	0.1136		Yes

Figure 1b – Identify AODE5271RI Sediment PIHS Selecting "Sort Largest to Smallest' in 'MaxDetect_Exceedance'

ChemicalName	MeasurementBasis	Criteria_Name	MinCriteriaValue	MaxDetect_Exceedance	MaxNonDetect_Exceedance	FreqOfDetection	FreqOfDetect_Exceedance	FreqOfNonDetect_Exceedance	Potential_IHS
arsenic	dry	R Soil_Meth B_Carc	0.67	3330	10.5	0.7519	0.7519	0.2481	Yes
chrysene	dry	R Soil_Meth B_Carc	0.14	50.37	1.898	0.6568	0.3136	0.005917	Yes
benzo(a)pyrene	dry	R Soil_Meth A_Unrestricted	0.1	34	4.1	0.6154	0.2899	0.01775	Yes
pcbs	dry	R Soil_Meth B_Carc	0.5	149.8	0.128	0.5763	0.2712		Yes
benzo(b)fluoranthene	dry	R Soil_Meth B_Carc	0.14	24.09	1.898	0.6272	0.2485	0.005917	Yes
benzo(k)fluoranthene	dry	R Soil_Meth B_Carc	0.14	24.09	1.898	0.6331	0.2485	0.005917	Yes
benz(a)anthracene	dry	R Soil_Meth B_Carc	0.14	36.5	2.993	0.6154	0.2367	0.01183	Yes
indeno(1,2,3-c,d)pyrene	dry	R Soil_Meth B_Carc	0.14	11.68	2.993	0.5799	0.1893	0.01183	Yes
aroclor 1254	dry	R Soil_Meth B_Non Carc	1.6	15.62	0.02062	0.5763	0.1525		Yes
lead	dry	R Soil_Meth A_Unrestricted	250	18.52	0.012	0.8968	0.1508		Yes
dibenzo(a,h)anthracene	dry	R Soil_Meth B_Carc	0.14	2.993	2.993	0.4556	0.1124	0.01775	Yes

Figure 1c – Identify AODE5271RI Soil PIHS Selecting 'Sort Largest to Smallest' in 'FreqOfDetect_Exceedance'

ChemicalName	MeasurementBasis	Criteria_Name	MinCriteriaValue	MaxDetect_Exceedance	MaxNonDetect_Exceedance	FreqOfDetection	FreqOfDetect_Exceedance	FreqOfNonDetect_Exceedance	Potential_IHS
arsenic	dry	R Soil_Meth B_Carc	0.67	3330	10.5	0.7519	0.7519	0.2481	Yes
pcbs	dry	R Soil_Meth B_Carc	0.5	149.8	0.128	0.5763	0.2712		Yes
chrysene	dry	R Soil_Meth B_Carc	0.14	50.37	1.898	0.6568	0.3136	0.005917	Yes
benz(a)anthracene	dry	R Soil_Meth B_Carc	0.14	36.5	2.993	0.6154	0.2367	0.01183	Yes
benzo(a)pyrene	dry	R Soil_Meth A_Unrestricted	0.1	34	4.1	0.6154	0.2899	0.01775	Yes
benzo(b)fluoranthene	dry	R Soil_Meth B_Carc	0.14	24.09	1.898	0.6272	0.2485	0.005917	Yes
benzo(k)fluoranthene	dry	R Soil_Meth B_Carc	0.14	24.09	1.898	0.6331	0.2485	0.005917	Yes
lead	dry	R Soil_Meth A_Unrestricted	250	18.52	0.012	0.8968	0.1508		Yes
aroclor 1254	dry	R Soil_Meth B_Non Carc	1.6	15.62	0.02062	0.5763	0.1525		Yes
indeno(1,2,3-c,d)pyrene	dry	R Soil_Meth B_Carc	0.14	11.68	2.993	0.5799	0.1893	0.01183	Yes
mercury	dry	R Soil_Meth A_Unrestricted	2	11	0.03	0.6763	0.07194		Yes
antimony	dry	R Soil_Meth B_Non Carc	32	10	0.9375	0.2101	0.1008		Yes
dibenzo(a,h)anthracene	dry	R Soil_Meth B_Carc	0.14	2.993	2.993	0.4556	0.1124	0.01775	Yes

Figure 1d – Identify AODE5271RI Soil PIHS Selecting "Sort Largest to Smallest' in 'MaxDetect_Exceedance'

Notes